

## SEQUENCE LISTING

<110> ERTL, Peter F.

<120> Vaccine

<130> PG5024

<140> Not Yet Assigned

<141> 2005-05-04

<150> PCT/EP2003/012429

<151> 2003-03-11

<150> GB 0225786.3

<151> 2002-11-05

<160> 106

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA primer

<400> 1

atcgtccatg ggtggcaagt ggt

23

<210> 2

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA primer

<400> 2

cggctactag tgcagttcct gaa

23

<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA primer

<400> 3

atcgtactag tgagccagta gatc

24

<210> 4

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA primer

<400> 4

cggctactag tttccttcgg gcct

24

seqlist.txt

<210> 5  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic DNA primer  
  
 <400> 5  
 gaattcgcg cgcgcattggg tggcaagtgg tcaaaaag 38  
  
 <210> 6  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic DNA primer  
  
 <400> 6  
 gaattcgcg cgcgcattggg gggttttcca gtcacacc 38  
  
 <210> 7  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic DNA primer  
  
 <400> 7  
 gaattcgga ccttattcct tcgggcctgt cggg 34  
  
 <210> 8  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic polylinker  
  
 <400> 8  
 agcttgcggc cgctagcgat atcggtacca tatgtcgacg gatcc 45  
  
 <210> 9  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic polylinker  
  
 <400> 9  
 gtaccggtca attggcgccg gcgcgccata tgacgtcaga tctg 44  
  
 <210> 10  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 10  
 ccatggatcc gatctttttc cctctgcc 28  
  
 <210> 11  
 <211> 32

seqlist.txt

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 11  
 gttagggtga aaagcttccg agtgagagac ac 32  
  
 <210> 12  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 12  
 gttagggtga aaagcttccg agtgagagac ac 32  
  
 <210> 13  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 13  
 gttctccatc gcggccgcac tcttggcacg ggg 33  
  
 <210> 14  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 14  
 gaattcgcg cgcctatggc cgagcagctg tgggtcacc 39  
  
 <210> 15  
 <211> 55  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 15  
 gaattcggat cctcatctct gcacgacgcg gcgcttggcc cgggtggggg ccacg 55  
  
 <210> 16  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 16  
 gccaaagcgcc gcgtcgtgca gaga 24  
  
 <210> 17  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

seqlist.txt

```

<220>
<223> Synthetic primer

<400> 17
gccaaagcgcc gcgtcgtgca gagaatgggt ggcaagtgggt caaaaagt      48

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 18
ggggagccga caggcccgaa ggaa      24

<210> 19
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 19
ggggagccga caggcccgaa ggaaatgaag gtcaaggaga ccagaaag      48

<210> 20
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 20
gccaaagcgcc gcgtcgtgca gagaatgggt gggtttccag tcac      44

<210> 21
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 21
gaattcgcg cgcctatggt ggggtttcca gtcacacc      38

<210> 22
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 22
gaattcggat cctcatctct gcacgacgcg gcgcttgGCC cgggtggggg ccacg      55

<210> 23
<211> 60
<212> DNA
<213> Artificial Sequence

<220>

```

<223> Synthetic primer

<400> 23  
accaccttgt acttgtagag ctcgctccgc cagttatccc tcatgtcgcc gccgccgggc 60

<210> 24

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 24  
gaattcgagg ccgcatgga gccagtagat cctagac 37

<210> 25

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 25  
ttccttcggg cctgtcggc 19

<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 26  
gccgacaggc ccgaaggaaa tggtaggggtt tccagtcaca c 41

<210> 27

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 27  
gaattcggat ccttagcagt tcttgaagta ctccgg 36

<210> 28

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

<400> 28  
gaattcggg ccgcaatgaa ggtcaaggag accagaaaga actaccagca tctgtg 56

<210> 29

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic primer

seqlist.txt

```

<400> 29
tctctgcacg acgcggcgct tggc 24

<210> 30
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 30
gccaaagcgc gcgtcgtgga gagaatgggt gcccgagctt cggtac 46

<210> 31
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 31
gaattcggat ccttagcagt tcttgaagta ctccgg 36

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 32
gccaaagcgc gcgtcgtgga gagaatgggt gcccgagctt cggtac 46

<210> 33
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 33
caacactctg gctttgtgtc c 21

<210> 34
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 34
ggacacaaag ccagagtgtt gatgggcaag tgggtcaaaaa gtag 44

<210> 35
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 35

```

```

                                seqlist.txt
gaattcggat ccttagcagt tcttgaagta ctccgg                                36
<210> 36
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 36
ggacacaaag ccagagtgtt gatgggcaag tgggtcaaaaa gtag                                44
<210> 37
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 37
gaattcgcgg ccgccatggg tggcaagtgg tcaaaaag                                38
<210> 38
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 38
gccataaag gagagaacac cagc                                24
<210> 39
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 39
gccataaag gagagaacac cagcgcctta caccctgtga gcctgcatg                                49
<210> 40
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 40
gccataaag gagagaacac cagcttggca caccctgtga gcctgcatg                                49
<210> 41
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer

<400> 41
gccataaag gagagaacac cagcgccgca caccctgtga gcctgcatg                                49

```

seqlist.txt

<210> 42  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 42  
 ggggagccga caggcccgaa ggaa 24  
  
 <210> 43  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 43  
 gaattcgcg cgcggcatggc cgagcagctg tgggtcacc 39  
  
 <210> 44  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 44  
 gccaaagcgcc gcgtcgtgca gaga 24  
  
 <210> 45  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 45  
 gccaaagcgcc gcgtcgtgca gagaatgggc cccatcagtc ccatc 45  
  
 <210> 46  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 46  
 cgtcacgatg ttcacctcca ggcc 24  
  
 <210> 47  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic primer  
  
 <400> 47  
 gtggcccagag agctgcatcc g 21  
  
 <210> 48  
 <211> 48



## seqlist.txt

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic primer

<400> 48  
 ggacacaaag ccagagtgtt gatggccgag cagctgtggg tcaccgtc

48

<210> 49  
 <211> 514  
 <212> PRT  
 <213> HIV-1

<400> 49  
 Met Lys Val Lys Glu Thr Arg Lys Asn Tyr Gln His Leu Trp Arg Trp  
 1 5 10 15  
 Gly Thr Met Leu Gly Met Leu Met Ile Cys Ser Ala Ala Glu Gln  
 20 25 30  
 Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr  
 35 40 45  
 Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val  
 50 55 60  
 His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro  
 65 70 75 80  
 Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe Asn Met Trp Lys  
 85 90 95  
 Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp  
 100 105 110  
 Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu  
 115 120 125  
 Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr Thr Ser Asn  
 130 135 140  
 Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe  
 145 150 155 160  
 Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu  
 165 170 175  
 Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp Asn Ala Thr Thr  
 180 185 190  
 Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His Cys Asn Ser Ser  
 195 200 205  
 Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile  
 210 215 220  
 His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys  
 225 230 235 240  
 Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser Thr Val Gln Cys  
 245 250 255  
 Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly  
 260 265 270  
 Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp Asn Phe Met Asp  
 275 280 285  
 Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Ala Ile Asn  
 290 295 300  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro  
 305 310 315 320  
 Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly Asp Ile Arg Gln  
 325 330 335  
 Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn Thr Leu Lys Gln  
 340 345 350  
 Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys Thr Ile Lys Phe  
 355 360 365  
 Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg His Ser Phe Asn  
 370 375 380  
 Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln Leu Phe Asn Ser  
 385 390 395 400  
 Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly Asn Ser Thr Ile  
 405 410 415  
 Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val

seqlist.txt

Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln	Ile	Arg	Cys	Ser
		435					440					445			
Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Thr	Glu	Gly
	450					455					460				
Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro	Gly	Gly	Gly	Asp
465					470					475					480
Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys
				485					490					495	
Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys	Arg	Arg	Val	Val
			500					505					510		
Gln	Arg														

<210> 50  
 <211> 1545  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Codon optimised DNA for gp120

<400> 50  
 atgaaggtca aggagaccag aaagaactac cagcatctgt ggcgctgggg caccatgctc 60  
 ctgggaatgc tgatgatctg ctccgccgcc gagcagctgt gggtcaccgt ctactacggc 120  
 gtgcctgtgt ggaaggaggc cacgaccacc ctcttctgcg cgagcgacgc caaggcctac 180  
 gacacggaag tgcataacgt gtgggcgacg catgcttgcg tgcctacgga cccaacccc 240  
 caggaggtgg tgctgggaaa cgtgaccgag tacttcaaca tgtggaagaa taacatggtg 300  
 gatcagatgc acgaggacat catctctctg tgggaccagt ccctgaagcc ctgctgaag 360  
 ctgacgcctc tctgctgac actggactgt gacgacgtca acaccaccaa cagcactacc 420  
 accaccagca acggctggac cggagagatt cggaaggcg agatcaagaa ctgctccttc 480  
 aatatcacga cctcgatcag agacaagggt cagaaggaa acgcgctgtt ttataatctc 540  
 gatgtggtcc ccacgacga cgacaatgcc accaccaaga acaagacgac gcgtaatttc 600  
 agatcattc actgcaacag cagcgtcatg acgcaggcct gccccaaagg gtccttcgaa 660  
 ccaatcccga tccattactg tgcccctgcc ggattcgcga tcctcaagt taacaacaag 720  
 accttcgacg ggaaggccct gtgcaccaac gtcagcacgg tgcagtgac ccatggcatc 780  
 cgccccgtcg tgagcaccca gctgctgctg aacgggtccc tggctgagga ggaggtggtg 840  
 atccggtcgg acaacttcat ggacaacacc aagacaatca tcgtccagct gaacgagtct 900  
 gtggcgatta actgtaccgg gcctaacaac aacaccgta agggcatcca catcgggcct 960  
 ggacgggcct tctatgccgc ccgcaagat atcggcgaca tccggcaggc ccattgcaac 1020  
 ctctcccgcg cccagtggaa taacaccctg aagcagatcg tgatcaagct gagagagcac 1080  
 tttggaacaa agaccatcaa gttcaatcag agttctggcg gagaccccga gatcgtgcgg 1140  
 cactccttca actgcggggg cgagttcttc tactgcgata cgacacagct cttcaactcc 1200  
 acctggaacg gcaccgaggc caacaacaca gagggaaact ccactatcac cctcccttgc 1260  
 cgcataacag agatcatcaa catgtggcag gaggtgggaa aggccatgta tgccccccc 1320  
 atcgggggccc agatccgctg ctccctcaac atcaccggcc tgctgctcac cagagacggg 1380  
 ggcaccgagg gcaacggcac ggagaacgag acggagatct tcaggcccgg cggcggcgac 1440  
 atgagggata actggcggag cgagctgtac aagtacaagg tgggtgaagg ggagccgctc 1500  
 ggcgtggccc ccacccgggc caagcgcgcg gtcgtgcaga gatga 1545

<210> 51  
 <211> 882  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 Nef-Tatm fusion

<400> 51  
 atgggtggca agtgggtcaaa aagtagtggt gttggatggc ctactgtaag ggaaagaatg 60  
 agacgagctg agccagcagc agatgggggt ggagcagcat ctcgagacct ggaaaaacat 120  
 ggagcaatca caagtagcaa tacagcagct accaatgctg cttgtgcctg gctagaagca 180  
 caagaggagg aggaggtggg ttttcagtc acacctcagg tacctttaag accaatgact 240  
 tacaaggcag ctgtagatct tagccacttt ttaaaagaaa aggggggact ggaagggtta 300  
 attcactccc aacgaagaca agatatcctt gatctgtgga tctaccacac acaaggctac 360  
 ttccctgatt ggcagaacta cacaccagg ccagggggtc gatatccact gacccttgga 420  
 tgggtgctaca agctagtagc agttgagcca gataaggtag aagaggccaa taaaggagag 480

seqlist.txt

```
aacaccagct tgttacaccc tgtgagcctg catggaatgg atgaccctga gagagaagtg 540
ttagagtggg ggtttgacag ccgcctagca ttatcatcac tggcccgaga gctgcatccg 600
gagtacttca agaactgcac tagtgagcca gtagatccta gactagagcc ctggaagcat 660
ccaggaagtc agcctaaaac tgcttgtagc aattgctatt gtaaaaagtg ttgctttcat 720
tgccaagttt gtttcataac agctgcctta ggcattctct atggcaggaa gaagcggaga 780
cagcgacgaa gacctcctca aggcagtcag actcatcaag tttctctatc aaagcaaccc 840
acctcccaat ccaaagggga gccgacaggc ccgaaggaat aa 882
```

<210> 52  
 <211> 293  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 Nef-Tatm fusion

<400> 52  
 Met Gly Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val  
 1 5 10 15  
 Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala  
 20 25 30  
 Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Asn Thr  
 35 40 45  
 Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu  
 50 55 60  
 Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr  
 65 70 75 80  
 Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly  
 85 90 95  
 Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu  
 100 105 110  
 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr  
 115 120 125  
 Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys  
 130 135 140  
 Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu  
 145 150 155 160  
 Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro  
 165 170 175  
 Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His  
 180 185 190  
 His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser  
 195 200 205  
 Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln  
 210 215 220  
 Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His  
 225 230 235 240  
 Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg  
 245 250 255  
 Lys Lys Arg Arg Gln Arg Arg Arg Pro Gln Gly Ser Gln Thr His  
 260 265 270  
 Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro  
 275 280 285  
 Thr Gly Pro Lys Glu  
 290

<210> 53  
 <211> 690  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 trNef-Tatm fusion

<400> 53  
 atggtgggtt ttccagtcac acctcaggtg cttttaagac caatgactta caaggcagct 60  
 gtatgacttta gccacttttt aaaagaaaag gggggactgg aagggctaata tcaactccaa 120  
 Page 11

seqlist.txt

```
cgaagacaag atattccttga tctgtggatc taccacacac aaggctactt ccctgattgg 180
cagaactaca caccagggcc aggggtcaga tatccactga cctttggatg gtgctacaag 240
ctagtaccag ttgagccaga taaggtagaa gaggccaata aaggagagaa caccagcttg 300
ttacaccctg tgagcctgca tggaatggat gaccctgaga gagaagtgtt agagtggagg 360
tttgacagcc gcctagcatt tcatcacgtg gcccgagagc tgcattccgga gtacttcaag 420
aactgcacta gtgagccagt agatccctaga ctagagccct ggaagcatcc aggaagtccag 480
cctaaaactg cttgtaccaaa ttgctattgt aaaaagtgtt gctttcattg ccaagtttgt 540
ttcataacag ctgccttagg catctcctat ggcaggaaga agcggagaca gcgacgaaga 600
cctcctcaag gcagtcagac tcatcaagtt tctctatcaa agcaaccac ctcccaatcc 660
aaaggggagc cgacaggccc gaaggaataa 690
```

<210> 54  
 <211> 229  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 trNef-Tatm fusion

```
<400> 54
Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
1 5 10 15
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
20 25 30
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
35 40 45
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
50 55 60
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
65 70 75 80
Leu Val Pro Val Glu Pro Asp Lys Val Glu Ala Asn Lys Gly Glu
85 90 95
Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
100 105 110
Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
115 120 125
His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
130 135 140
Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
145 150 155 160
Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
165 170 175
Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
180 185 190
Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His
195 200 205
Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro
210 215 220
Thr Gly Pro Lys Glu
225
```

<210> 55  
 <211> 1461  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c

```
<400> 55
atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60
accaccctct tctgcgcgag cgacgccaaag gcctacgaca cggaagtgca taactgtgtg 120
gcgacgcctg cttgcgtgcc tacggacccc aaccccagg aggtggtgct gggaaaacgtg 180
accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtcctt gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420
```

seqlist.txt

```

aaggtgcaga aggaataacgc gctgttttat aatctcgatg tgggtcccat cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
gtcatgacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600
cctgccggat tcgcatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660
accaacgtca gcacgggtgca gtgacccat ggcattccgcc ccgtcgtgag caccagctg 720
ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccggccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
aatcagagtt ctggcggaga ccccgagatc gtgcggcact ccttcaactg cggggcgag 1080
ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggcaac 1140
aacacagagg gaaactccac tatcaccctc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc cccccatcg gggggccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gccggcggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaagggtgg gaaggtggag ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgtcg tgcagagatg a

```

<210> 56

<211> 486

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c

<400> 56

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235      240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315      320

```

seqlist.txt

Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys
				325					330					335	
Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg
			340					345					350		
His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
		355					360					365			
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
	370					375					380				
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
	385				390					395					400
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
			405						410					415	
Ile	Arg	Cys	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	
			420				425						430		
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
		435					440					445			
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
	450					455					460				
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys
	465				470					475					480
Arg	Arg	Val	Val	Gln	Arg										
				485											

<210> 57  
 <211> 2340  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c'

<400> 57

atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaag	gcctacgaca	cggaagtgc	taacgtgtgg	120
gcgacgcatg	cttgcgtgcc	tacggacccc	aacccccagg	agggtgtgct	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atgggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtcctt	gaagccctgc	gtgaagctga	cgcctctctg	cgtgacactg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaatacgc	gctgttttat	aatctcgtatg	tggtcccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caagggtgcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgcccgat	tcgcgatcct	caagtgtaac	aacaagacct	tcgacgggaa	gggcctgtgc	660
accaacgtca	gcacggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	caccagctg	720
ctgtctgaacg	ggtccttgcc	tgaggaggag	gtggtgatcc	ggtcggacaa	cttcattggac	780
aacaccaaga	caatcatcgt	ccagctgaac	gagctgtgtg	cgattaactg	tacccggcct	840
aacaacaaca	cccgtgaagg	catccacatc	gggcctggac	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccat	tgcaacctct	cccgcgcca	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcagagtt	ctggcggaga	ccccgagatc	gtgcggcact	ccttcaactg	cgggggcgag	1080
ttcttctact	gcgatacgac	acagctcttc	aactccacct	ggaacggcac	cgagggcaac	1140
aacacagagg	gaaactccac	tatcacccctc	ccttgccgca	tcaagcagat	catcaacatg	1200
tggcaggagg	tgggaaaggc	catgtatgcc	ccccccatcg	ggggccagat	ccgctgctcc	1260
tccaacatca	ccggcctgct	gctcaccaga	gacgggggca	ccgagggcaa	cggcacggag	1320
aacgagacgg	agatcttcag	gcccggcggc	ggcgacatga	gggataactg	gcggagcgag	1380
ctgtacaagt	acaaggtggg	gaaggtggag	ccgctcggcg	tggcccccac	ccgggccaag	1440
cgccgcgtcg	tgcagagaat	gggtggcaag	tggtcaaaaa	gtagtgtggg	tggatggcct	1500
actgtaaggg	aaagaatgag	acgagctgag	ccagcagcag	atgggggtggg	agcagcatct	1560
cgagacctgg	aaaaacatgg	agcaatcaca	agtagcaata	cagcagctac	caatgctgct	1620
tgtgcctggc	tagaagcaca	agaggaggag	gaggtggggt	ttccagtcac	acctcaggta	1680
cctttaagac	caatgactta	caaggcagct	gtagatctta	gccacttttt	aaaagaaaag	1740
gggggactgg	aagggttaat	tcactcccaa	cgaagacaag	atataccttg	tctgtggatc	1800
taccacacac	aaggctactt	ccctgattgg	cagaactaca	caccagggcc	aggggtcaga	1860
tatccactga	cctttggatg	gtgtacaaag	ctagtaccag	ttgagccaga	taaggtagaa	1920
gaggccaata	aaggagagaa	caccagcttg	ttacaccctg	tgagcctgca	tggaatggat	1980
gaccctgaga	gagaagtgtt	agagtggagg	tttgacagcc	gcctagcatt	tcatcacgtg	2040
gcccagagagc	tgcattccgga	gtacttcaag	aactgcacta	gtgagccagt	agatccctaga	2100

seqlist.txt

ctagagccct ggaagcatcc aggaagtcag cctaaaactg cttgtaccaa ttgctattgt 2160  
 aaaaagtgtt gctttcattg ccaagtttgt ttcataacag ctgccttagg catctcctat 2220  
 ggcaggaaga agcggagaca gcgacgaaga cctcctcaag gcagtcagac tcatcaagtt 2280  
 tctctatcaa agcaaccac ctcccaatcc aaaggggagc cgacaggccc gaaggaataa 2340

<210> 58  
 <211> 779  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c'

<400> 58  
 Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp  
 1 5 10 15  
 Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr  
 20 25 30  
 Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr  
 35 40 45  
 Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe  
 50 55 60  
 Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile  
 65 70 75 80  
 Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu  
 85 90 95  
 Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr  
 100 105 110  
 Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys  
 115 120 125  
 Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys  
 130 135 140  
 Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp  
 145 150 155 160  
 Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His  
 165 170 175  
 Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu  
 180 185 190  
 Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys  
 195 200 205  
 Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser  
 210 215 220  
 Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu  
 225 230 235 240  
 Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp  
 245 250 255  
 Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser  
 260 265 270  
 Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile  
 275 280 285  
 His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly  
 290 295 300  
 Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn  
 305 310 315 320  
 Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys  
 325 330 335  
 Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg  
 340 345 350  
 His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln  
 355 360 365  
 Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly  
 370 375 380  
 Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met  
 385 390 395 400  
 Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln  
 405 410 415  
 Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Thr Arg Asp Gly

seqlist.txt

			420					425					430				
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro		
		435					440					445					
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr		
	450					455					460						
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys		
465					470					475					480		
Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Gly	Lys	Trp	Ser	Lys	Ser	Ser	Val		
				485					490					495			
Val	Gly	Trp	Pro	Thr	Val	Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala		
			500					505					510				
Ala	Asp	Gly	Val	Gly	Ala	Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala		
	515						520					525					
Ile	Thr	Ser	Ser	Asn	Thr	Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu		
	530					535					540						
Glu	Ala	Gln	Glu	Glu	Glu	Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val		
545					550					555					560		
Pro	Leu	Arg	Pro	Met	Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe		
				565					570					575			
Leu	Lys	Glu	Lys	Gly	Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg		
			580					585					590				
Gln	Asp	Ile	Leu	Asp	Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro		
	595						600					605					
Asp	Trp	Gln	Asn	Tyr	Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr		
	610					615					620						
Phe	Gly	Trp	Cys	Tyr	Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu		
625					630					635					640		
Glu	Ala	Asn	Lys	Gly	Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu		
				645					650					655			
His	Gly	Met	Asp	Asp	Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp		
			660					665					670				
Ser	Arg	Leu	Ala	Phe	His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr		
			675				680					685					
Phe	Lys	Asn	Cys	Thr	Ser	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp		
	690					695					700						
Lys	His	Pro	Gly	Ser	Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys		
705					710					715					720		
Lys	Lys	Cys	Cys	Phe	His	Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	Leu		
				725					730					735			
Gly	Ile	Ser	Tyr	Gly	Arg	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro		
			740					745					750				
Gln	Gly	Ser	Gln	Thr	His	Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser		
		755					760					765					
Gln	Ser	Lys	Gly	Glu	Pro	Thr	Gly	Pro	Lys	Glu							
	770					775											

<210> 59  
 <211> 2148  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c trNef-Tatm fusion

<400> 59																	
atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60											
accaccctct	tctgcgcgag	cgacgccaag	gcctacgaca	cggaagtgc	taacgtgtg	120											
gcgacgcatt	cttgcgtgcc	tacggacccc	aacccccagg	agggtgtgct	gggaaacgtg	180											
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240											
tctctgtggg	accagtcctt	gaagccctgc	gtgaagctga	cgcctctctg	cgtgacactg	300											
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360											
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420											
aaggtgcaga	aggaatacgc	gctgttttat	aattctcgatg	tggtccccc	cgacgacgac	480											
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540											
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600											
cctgccggat	tcgcgatcct	caagtgtaac	aacaagacct	tcgacgggaa	gggcctgtgc	660											
accaacgtca	gcacggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	caccagctg	720											



seqlist.txt

```

ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccgcgcct 840
aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgcccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
aatcagagtt ctggcggaga ccccgagatc gtgcggcact ccttcaactg cgggggcgag 1080
ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggcaac 1140
aacacagagg gaaactccac tatcaccctc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc ccccccacg ggggccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gccggcgggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaagggtgg gaaggtggag ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgtcg tgcagagaat ggtgggtttt ccagtcacac ctgaggtacc tttaagacca 1500
atgacttaca aggcagctgt agatcttagc cactttttaa aagaaaaggg gggactggaa 1560
gggctaattc actcccaacg aagacaagat atccttgatc tgtggatcta ccacacacaa 1620
ggctacttcc ctgattggca gaactacaca ccagggccag gggtcagata tccactgacc 1680
tttgatgggt gctacaagct agtaccagtt gagccagata aggtagaaga ggccaataaa 1740
ggagagaaca ccagcttggt acaccctgtg atgcctgcag gaatggatga cctgagaga 1800
gaagtgttag agtggaggtt tgacagccgc ctgacttttc atcacgtggc ccgagagctg 1860
catccggagt acttcaagaa ctgcactagt gagccagtag atcctagact agagccctgg 1920
aagcatccag gaagtcagcc taaaactgct tgtaccaatt gctattgtaa aaagtgttgc 1980
tttcattgcc aagtttggtt cataacagct gccttaggca tctcctatgg caggaagaag 2040
cgagatcgc gacgaagac tctcagagc agtcagactc atcaagttt tctatcaag 2100
caaccacct cccaatccaa aggggagccg acaggccga aggaataa 2148

```

<210> 60  
 <211> 715  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c trNef-Tatm fusion

```

<400> 60
Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20     25     30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35     40     45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50     55     60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65     70     75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85     90     95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100    105    110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115    120    125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130    135    140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145    150    155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165    170    175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180    185    190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195    200    205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210    215    220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225    230    235
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245    250    255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260    265    270

```

## seqlist.txt

```

Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
      275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
      290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315      320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
      325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Asp Pro Glu Ile Val Arg
      340      345      350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
      355      360      365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Thr Glu Gly
      370      375      380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
385      390      395      400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
      405      410      415
Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
      420      425      430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
      435      440      445
Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
      450      455      460
Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
465      470      475      480
Arg Arg Val Val Gln Arg Met Val Gly Phe Pro Val Thr Pro Gln Val
      485      490      495
Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe
      500      505      510
Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg
      515      520      525
Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro
      530      535      540
Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr
545      550      555      560
Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu
      565      570      575
Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu His Pro Val Ser Leu
      580      585      590
His Gly Met Asp Asp Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp
      595      600      605
Ser Arg Leu Ala Phe His His Val Ala Arg Glu Leu His Pro Glu Tyr
      610      615      620
Phe Lys Asn Cys Thr Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp
625      630      635      640
Lys His Pro Gly Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys
      645      650      655
Lys Lys Cys Cys Phe His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu
      660      665      670
Gly Ile Ser Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Pro Pro
      675      680      685
Gln Gly Ser Gln Thr His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser
      690      695      700
Gln Ser Lys Gly Glu Pro Thr Gly Pro Lys Glu
705      710      715

```

&lt;210&gt; 61

&lt;211&gt; 1887

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; HIV-1 ds-gp120c trNef fusion

&lt;400&gt; 61

atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60

seqlist.txt

```

accaccctct tctgcgcgag cgacgccaag gcctacgaca cggaagtgca taacgtgtgg 120
gcgacgcatg cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180
accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtcctt gaagccctgc gtgaagtga cgctctctg cgtgacactg 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420
aaggtgcaga aggaatacgc gctgttttat aatctcgatg tggccccat cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
gtcatgacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600
cctgccggat tcgcatcctt caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660
accaacgtca gcacggtgca gtgcacccat ggcattccgc ccgtcgtgag caccagctg 720
ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
aacaacaaca cccgtaaggg catccacatc ggcctggac gggccttcta tgccgccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcatttgc gaaacaagac catcaagttc 1020
aatcagagtt ctggcggaga ccccgagatc gtgcggcact ccttcaactg cgggggag 1080
ttcttctact gcgatacgc acagctcttc aactccacct ggaacggcac cgagggaac 1140
aacacagagg gaaactccac tatcaccctc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc ccccccacgc ggggccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaagggtgg gaaggtggag ccgctcggcg tggccccac ccgggccaag 1440
cgccgcgtcg tgcagagaat ggtgggtttt ccagtcacac ctcagggtacc tttaagacca 1500
atgacttaca aggcagctgt agatcttagc cactttttta aagaaaaggg gggactggaa 1560
gggctaattc actcccaacg aagacaagat atccttgatc tgtggatcta ccacacaaa 1620
ggctacttcc ctgattggca gaactacaca ccagggccag gggtcagata tccactgacc 1680
tttgatgggt gctacaagct agtaccagtt gagccagata aggtagaaga ggccaataaa 1740
ggagagaaca ccagcttgtt acaccctgtg agcctgcatg gaatggatga ccctgagaga 1800
gaagtgttag agtggagggt tgacagccgc ctagcatttc atcacgtggc ccgagagctg 1860
catccggagt acttcaagaa ctgctaa 1887

```

<210> 62

<211> 628

<212> PRT

<213> Artificial sequence

<220>

<223> HIV-1 ds-gp120c trNef fusion

<400> 62

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
 1      5      10     15
Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
      20     25     30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
      35     40     45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
      50     55     60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
      65     70     75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
      85     90     95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
      100    105    110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
      115    120    125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
      130    135    140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
      145    150    155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
      165    170    175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
      180    185    190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
      195    200    205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser

```

## seqlist.txt

[illegible]

```
<210> 63
<211> 1517
<212> DNA
<213> Artificial sequence
```

<220>  
<223> HIV-1 Nef p17/24 fusion

<400>	63						
tgggtgcccc	agcttcggtg	ctgtctggtg	gagagctgga	cagatgggag	aaaattaggc	60	
tgcgcccggg	aggcaaaaag	aaatacaagc	tcaagcatat	cgtgtggggc	tcgagggagc	120	
ttgaacgggt	tgcctgtgaac	ccaggcctgc	tggaaacatc	tgagggatgt	cgccagatcc	180	
tggcgcaatt	gcagccattc	ctccagaccg	ggagtgaaga	gctgaggttc	ttgtataaca	240	

seqlist.txt

```

cagtggctac cctctactgc gtacaccaga ggatcgagat taaggatacc aaggaggcct 300
tggaacaaat tgaaggaggag caaaacaaga gcaagaagaa ggcccagcag gcagctgctg 360
acactgggca tagcaaccag gtatcacaga actatcctat tgtccaaaac attcagggcc 420
agatgggttca tcaggccatc agcccccgga cgctcaatgc ctgggtgaag gttgtcgaag 480
agaaggcctt ttctcctgag gttatcccca tgttctcgc tttgagttag ggggccactc 540
ctcaggacct caatacaatg cttaataaccg tgggcggcc tcaggccgcc atgcaaagt 600
tgaaggagac tatcaacgag gaggcagccg agtgggacag agtgcattcc gtccacgctg 660
gccaatcgc gcccgagacg atgcgggagc ctgcgggctc tgacattgcc ggcaccacct 720
ctacactgca agagcaaatc ggatggatga ccaacaatcc tcccatccca gttggagaaa 780
tctataaacg gtggatcatt ctcggtctca ataaaattgt tagaatgtac tctccgacat 840
ccatccttga cattagacag ggacccaaag agccttttag ggattacgtc gaccggtttt 900
ataagacctt gcgagcagag caggcctctc aggaggtcaa aaactggatg acggagacac 960
tcctggtaca gaacgctaag cccgactgca aaacaattct gaaggcacta ggcccggctg 1020
ccaccctgga agagatgatg accgctgtc agggagtagg cggacccgga cacaagcca 1080
gagtgttgat ggtgggtttt ccagtcacac ctgaggtacc ttttaagacca atgacttaca 1140
aggcagctgt agatcttagc cactttttaa aagaaaaggg gggactggaa gggctaattc 1200
actcccaaag aagacaagat atccttgatc tgtggatcta ccacacacaa ggctacttcc 1260
ctgattggca gaactacaca ccagggccag gggtcagata tccactgacc ttggtatggt 1320
gtacaagct agtaccagtt gagccagata aggtagaaga ggccaataaa ggagagaaca 1380
ccagcttggt acaccctgtg agcctgcatg ggatggatga cccggagaga gaagtgttag 1440
agtggaggtt tgacagccgc ctgacatttc atcacgtggc ccgagagctg catccggagt 1500
acttcaagaa ctgctga 1517

```

<210> 64

<211> 2976

<212> DNA

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 trNef fusion

<400> 64

```

atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60
accaccctct tctgcgcgag cgacgccaaag gcctacgaca cggaagtgc taactgtgtg 120
gcgacgcatg cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180
accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240
tctctgtggg gaagccctgc gaagccctgc actaccacca ccagcaacgg ctggaccgga 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420
aaggtgcaga aggaatacgc gctgttttat aatctcgatg tgggtccccat cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
gtcatgacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600
cctgcccgat tcgcatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660
accaacgtca gcacggtgca gtgcacccat ggcattccgc ccgtcgtgag caccagctg 720
ctgtgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga ccagctgagc ccagctgagc gagctgtggy cgattaaactg taccggcct 840
aacaacaaca cccgtaaggc catccacatc gggcctggac gggccttcta tgccgcccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcatttg gaaacaagac catcaagttc 1020
aatcagagtt ctggcggaga ccccgagatc gtgcggcact ctttcaactg cgggggcgag 1080
ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggcaac 1140
aacacagagg gaaactccac tatcacctc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc ccccccacg ggggccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gcccgcgccg ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaaggtggg gaaggtggag ccgctcggcg tggccccac ccgggccaag 1440
cgccgcgtcg tgcagagaat ggggtgccga gcttcggtac tgtctggtgg agagctggac 1500
agatgggaga aaattaggct gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560
gtgtgggcct cgagggagct tgaacggttt gccgtgaacc caggcctgct ggaaacatct 1620
gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680
ctgaggtcct tgtataacac agtggctacc ctactactgc tacaccagag gatcgagatt 1740
aaggatacca aggaggcctt ggacaaaatt gaggaggagc aaaacaagag caagaagaag 1800
gcccagcagg cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860
gtccaaaaa ttcagggcca gatggttcac caggccatca gccccggac gctcaatgcc 1920
tgggtgaagg ttgtcgaaga gaaggccttt tctctgagg ttatccccat gttctccgct 1980
ttgagttagg gggccactcc tcaggacctc aataaatgc ttaataaccgt gggcggccat 2040
caggccgcca tgcaaatgtt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100
gtgcatcccg tccacgctgg cccaatcgcg cccggacaga tgcgggagcc tcgcggtctc 2160

```

seqlist.txt

```

gacattgccg gcaccacctc tacactgcaa gagcaaatacg gatggatgac caacaatcct 2220
cccatccagc ttggagaaat ctataaacgg tggatcattc tcgggtctcaa taaaattggt 2280
agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340
gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggaggtcaaa 2400
aactggatga cggagacact cctgggtacag aacgctaacc ccgactgcaa aacaatcttg 2460
aaggcactag gcccggctgc caccctggaa gagatgatga ccgcctgtca gggagtaggc 2520
ggaccgagac acaaagccag agtggtgatg gtgggttttc cagtcacacc tcaggtacct 2580
ttaagaccaa tgacttacaa ggcagctgta gatcttagcc actttttaaa agaaaagggg 2640
ggactggaag ggctaattca ctccaacga agacaagata tccttgatct gtggatctac 2700
cacacacaag gctacttccc tgattggcag aactacacac cagggccagg ggtcagatat 2760
ccactgacct ttggatggtg ctacaagcta gtaccagttg agccagataa ggtagaagag 2820
gccataaag gagagaacac cagcttgta caccctgtga gcctgcatgg aatggatgac 2880
cctgagagag aagtgttaga gtggagggtt gacagccgcc tagcatttca tcacgtggcc 2940
cgagagctgc atccggagta cttcaagaac tgctaa 2976

```

<210> 65

<211> 991

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 trNef fusion

<400> 65

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
 1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
 20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
 35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
 50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
 65      70      75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
 85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340      345      350

```

## seqlist.txt

His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
		355					360					365			
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
	370					375					380				
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
385					390					395					400
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
				405					410					415	
Ile	Arg	Cys	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	
			420				425					430			
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
		435					440					445			
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
		450				455					460				
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys
465					470					475					480
Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly
				485					490					495	
Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys
			500					505					510		
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu
		515					520					525			
Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg
	530					535					540				
Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu
545					550					555					560
Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln
				565					570					575	
Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu
			580					585					590		
Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr
		595					600					605			
Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile
	610					615					620				
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala
625					630					635					640
Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro
				645					650					655	
Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr
			660					665					670		
Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys
		675					680					685			
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val
	690				695						700				
His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser
705					710					715					720
Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met
				725					730					735	
Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile
			740					745					750		
Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile
		755					760					765			
Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp
	770					775					780				
Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys
785					790					795					800
Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys
				805					810					815	
Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met
			820					825					830		
Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val
		835					840					845			
Leu	Met	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met
	850					855					860				
Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly
865					870					875					880
Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp
				885					890					895	

seqlist.txt

Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr
			900					905					910		
Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr
		915					920					925			
Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly
	930					935					940				
Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp
945				950						955				960	
Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe
			965						970					975	
His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	
			980					985					990		

<210> 66  
 <211> 3237  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 trNef Tatm fusion

<400> 66

atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaag	gcctacgaca	cggaagtgc	taacgtgtgg	120
gcgacgcatt	cttgcggtgc	tacggacccc	aacccccagg	aggtgtgtgt	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtccct	gaagccctgc	gtgaagctga	cgctctctct	ctgtgacctg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaatacgc	gctgttttat	aatctcgtat	tggtcccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgctg	aatcttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgcccgat	tgcgcatcct	caagtgtaac	aacaagacct	tcgacgggaa	gggcctgtgc	660
accaacgtca	gcacgggtgc	gtgcacccat	ggcatccgcc	ccgtcgtgag	cacccagctg	720
ctgctgaacg	ggtcccttgc	tgaggaggag	gtggtgatcc	ggtcggacaa	cttcatggac	780
aacaccaaga	caatcatcgt	ccagctgaac	gagctctgtg	cgattaactg	taccggcct	840
aacaacaaca	cccgtgaagg	catccacatc	gggcctggac	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccat	tgcaacctct	cccgcgcca	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcacaggt	ctggcggaga	ccccgagatc	gtgcggcact	ccttcaactg	cgggggcgag	1080
ttcttctact	gcgatacgac	acagctcttc	aactccacct	ggaacggcac	cgagggcaac	1140
aacacagagg	gaaactccac	tatcaccttc	ccttgccgca	tcaagcagat	catcaacatg	1200
tggcaggagg	tgggaaaggc	catgtatgcc	cccccatcgc	ggggccagat	ccgctgctcc	1260
tccaacatca	ccggcctgct	gctcaccaga	gacgggggca	ccgagggcaa	cggcacggag	1320
aacgagacgg	agatcttcag	gcccggcggc	gccgacatga	gggataactg	gcggagcgag	1380
ctgtacaagt	acaagggtgt	gaaggtggag	ccgctcggcg	tggcccccac	ccgggccaag	1440
cgccgcgtcg	tgcagagaat	gggtgccgga	gcttcggtac	tgtctggtgg	agagctggac	1500
agatgggaga	aaattaggct	gcgcccggga	ggcaaaaaga	aatacaagct	caagcatatc	1560
gtgtgggcct	cgagggagct	tgaacggttt	gccgtgaacc	caggcctgct	ggaaacatct	1620
gagggatgtc	gccagatcct	ggggcaattg	cagccatccc	tccagaccgg	gagtgaagag	1680
ctgaggtcct	tgtataacac	agtggctacc	ctctactgcg	tacaccagag	gatcgagatt	1740
aaggatacca	aggaggcctt	ggacaaaatt	gaggaggagc	aaaacaagag	caagaagaag	1800
gcccagcagg	cagctgtctg	cactgggcat	agcaaccagg	tatcacagaa	ctatcctatt	1860
gtccaaaaca	ttcagggcca	gatggttcac	caggccatca	gccccgggac	gctcaatgcc	1920
tgggtgaagg	ttgtcgaaga	gaaggccttt	tctcctgagg	ttatccccat	gttctccgct	1980
ttgagtgaag	gggcccactc	tcaggacctc	aatacaatgc	ttaataccgt	gggcggccat	2040
caggccgcca	tgcaaatgtt	gaaggagact	atcaacgagg	aggcagccga	gtgggacaga	2100
gtcatctccg	tccacgtctg	cccaatcgcg	cccggacaga	tgcgggagcc	tcgcggtctc	2160
gacattgccg	gcaccacctc	tacactgcga	gagcaaatcg	gatggatgac	caacaatcct	2220
cccatccag	ttggagaaat	ctataaacgg	tggatcattc	tcggtctcaa	taaaattgtt	2280
agaatgtact	ctccgacatc	catccttgac	attagacagg	gacccaaaga	gccttttagg	2340
gattacgtcg	accggtttta	taagaccctg	cgagcagagc	aggcctctca	ggaggtcaaa	2400
aactgtatga	gggagacact	cctggtacag	aacgctaac	ccgactgcaa	aacaatcttg	2460
aaggcactag	cccgggctgc	caccctggaa	gagatgatga	ccgcctgtca	gggagttagc	2520
ggacccggac	acaaagccag	agtgttgatg	gtgggttttc	cagtcacacc	tcaggtacct	2580
ttaagaccaa	tgacttacaa	ggcagctgta	gatcttagcc	actttttaaa	agaaaagggg	2640
ggactggaag	ggctaattca	ctcccaacga	agacaagata	tccttgatct	gtggatctac	2700



seqlist.txt

```

cacacacaag gctacttccc tgattggcag aactacacac cagggccagg ggtagaatat 2760
ccactgacct ttggatgggtg ctacaagcta gtaccagttg agccagataa ggtagaagag 2820
gccataaag gagagaacac cagcttgta caccctgtga gcctgcatgg aatggatgac 2880
cctgagagag aagtgttaga gtggaggtt gacagccgc tagcatttca tcacgtggcc 2940
cgagagctgc atccggagta cttcaagaac tgcactagt agccagtaga tcctagacta 3000
gagccctgga agcatccagg aagtcagcct aaaactgctt gtaccaattg ctattgtaaa 3060
aagtgttgct ttcattgcca agtttgtttc ataacagctg ccttaggcat ctcctatggc 3120
aggaagaagc ggagacagcg acgaagacct cctcaaggca gtcagactca tcaagtttct 3180
ctatcaaagc aaccacacct ccaatccaaa ggggagccga caggcccga ggaataa 3237

```

<210> 67

<211> 1078

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 trNef Tatm fusion

<400> 67

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
 1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
 20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
 35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
 50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
 65      70      75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
 85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340      345      350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
355      360      365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly
370      375      380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met

```

## seq1ist.txt

```

385      390      395      400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
405      410      415
Ile Arg Cys Ser Asn Ile Thr Gly Leu Leu Thr Arg Asp Gly
420      425      430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
435      440      445
Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
450      455      460
Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
465      470      475      480
Arg Arg Val Val Gln Arg Met Gly Ala Arg Ala Ser Val Leu Ser Gly
485      490      495
Gly Glu Leu Asp Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys
500      505      510
Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu
515      520      525
Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr Ser Glu Cys Arg
530      535
Gln Ile Leu Gly Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu
545      550      555      560
Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln
565      570      575
Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu
580      585      590
Glu Gln Asn Lys Ser Lys Lys Ala Gln Gln Ala Ala Asp Thr
595      600      605
Gly His Ser Asn Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile
610      615      620
Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala
625      630      635      640
Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro
645      650      655
Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr
660      665      670
Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys
675      680      685
Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val
690      695      700
His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
705      710      715      720
Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
725      730      735
Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
740      745      750
Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
755      760      765
Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770      775      780
Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785      790      795      800
Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
805      810      815
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
820      825      830
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835      840      845
Leu Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met
850      855      860
Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly
865      870      875      880
Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp
885      890      895
Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr
900      905      910
Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr
915      920      925
Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly

```

seqlist.txt

930		935		940	
Glu Asn Thr Ser Leu	Leu His Pro Val Ser	Leu His Gly Met Asp			
945	950	955		960	
Pro Glu Arg Glu Val	Leu Glu Trp Arg Phe	Asp Ser Arg Leu Ala		Phe	
	965	970		975	
His His Val Ala Arg	Glu Leu His Pro	Glu Tyr Phe Lys Asn		Cys Thr	
	980	985		990	
Ser Glu Pro Val Asp	Pro Arg Leu Glu	Pro Trp Lys His		Pro Gly Ser	
	995	1000		1005	
Gln Pro Lys Thr Ala	Cys Thr Asn Cys Tyr	Cys Lys Lys Cys Cys		Phe	
	1010	1015		1020	
His Cys Gln Val Cys	Phe Ile Thr Ala Ala	Leu Gly Ile Ser Tyr		Gly	
1025	1030	1035		1040	
Arg Lys Lys Arg Arg	Gln Arg Arg Arg	Pro Pro Gln Gly Ser		Gln Thr	
	1045	1050		1055	
His Gln Val Ser Leu	Ser Lys Gln Pro	Thr Ser Gln Ser		Lys Gly Glu	
	1060	1065		1070	
Pro Thr Gly Pro Lys	Glu				
	1075				

<210> 68  
 <211> 3429  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 Nef Tatm fusion

<400> 68

atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaag	gcctacgaca	cggaagtgc	taacgtgtgg	120
gcgacgcatt	cttgcgtgcc	tacggacccc	aacccccagg	aggtggtgct	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtcctt	gaagccctgc	gtgaagctga	cgcctctctg	cgtgacactg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaatacgc	gctgttttat	aatctcgaat	tgggtcccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgcccgat	tcgcgatcct	caagtgtaac	aacaagacct	tcgacgggaa	gggacctgtc	660
accaacgtca	gcacggtgca	gtgcaccat	ggcatccgcc	ccgtcgtgag	caccagctg	720
ctgctgaacg	gggtccctgg	tgaggaggag	gtggtgatcc	ggtcggacaa	cttcatggac	780
aacaccaaga	caatcatcgt	ccagctgaac	gagtcgtgtg	cgattaactg	taccggtcct	840
aacaacaaca	cccgtaaagg	catccacatc	gggcctggac	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccc	tgcaacctct	cccgcgcccc	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcagagtt	ctggcggaga	ccccgagatc	gtgcggcact	ccttcaactg	cgggggcgag	1080
ttcttctact	gcgatacgac	acagctcttc	aactccacct	ggaacggcac	cgagggcaac	1140
aacacagagg	gaaactccac	tatcaccttc	ccttgccgca	tcaagcagat	catcaacatg	1200
tggcaggagg	tgggaaaggc	catgtatgcc	cccccatcgc	ggggccagat	ccgtgtctcc	1260
tccaacatca	ccggcctgct	gctcaccaga	gacgggggca	ccgagggcaa	cggcacggag	1320
aacgagacgg	agatcttcag	gcccggcggc	ggcgacatga	gggataactg	gcggagcgag	1380
ctgtacaagt	acaagggtgg	gaagggtggg	ccgctcggcg	tggcccccc	ccgggccaag	1440
cgccgcgtcg	tgcagagaat	gggtgcccga	gcttcggtac	tgtctggtgg	agagctggac	1500
agatgggaga	aaattaggct	gcgcccggga	ggcaaaaaga	aatacaagct	caagcatatc	1560
gtgtgggcct	cgaggagact	tgaacggttt	gccgtgaacc	caggcctgct	ggaaacatct	1620
gagggatgtc	gccagatcct	ggggcaattg	cagccatccc	tccagaccgg	gagtgaagag	1680
ctgaggtcct	tgtataaac	agtggctacc	cttactgctg	tacaccagag	gatcgagatt	1740
aaggatacca	aggagccctt	ggacaaaatt	gaggaggagc	aaaacaagag	caagaagaag	1800
gcccagcagg	cagctgctga	cactgggcat	agcaaccagg	tatcacagaa	ctatcctatt	1860
gtccaaaaca	ttcaggggca	gatgggttcat	caggccatca	gccccgggac	gctcaatgcc	1920
tgggtgaagg	ttgtcgaaga	gaaggccttt	tctcctgagg	ttatccccat	gttctccgct	1980
ttgagtgaag	ggggcactcc	tcaggacctc	aatacaatgc	ttaataaccg	gggcggccat	2040
caggccgcca	tgcaaatggt	gaaggagact	atcaacgagg	aggcagccga	gtgggacaga	2100
gtgcatcccc	tccacgctgg	cccaatcgcg	cccggacaga	tgcgggagcc	tcgcggtcct	2160
gacattgccg	gcaccacctc	tacactgcaa	gagcaaatcg	gatggatgac	caacaatcct	2220
cccatcccg	ttggagaaat	ctataaacgg	tggatcattc	tcggtctcaa	taaaattggt	2280

seqlist.txt

```

agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340
gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggaggtcaaa 2400
aactggatga cggagacact cctggtacag aacgctaacc ccgactgcaa aacaatcttg 2460
aaggcactag gcccggtgc caccctggaa gagatgatga ccgctgtca gggagttagc 2520
ggaccggac acaaagccag agtggtgatg ggtggcaagt ggtcaaaaag tagtgtggtt 2580
ggatggccta ctgtaaggga aagaatgaga cgagctgagc cagcagcaga tgggggtgga 2640
gcagcatctc gagacctgga aaaacatgga gcaatcaca gtagcaatac agcagctacc 2700
aatgctgctt gtgcctggct agaagcaca gagggaggag aggtgggttt tccagtcaca 2760
cctcaggtac ctttaagacc aatgacttac aaggcagctg tagatcttag ccacttttta 2820
aaagaaaagg ggggactgga agggctaatt cactcccaac gaagacaaga tatccttgat 2880
ctgtggatct accacacaca aggctacttc cctgattggc agaactacac accagggcca 2940
ggggtcagat atccactgac ctttggatgg tgctacaagc tagtaccagt tgagccagat 3000
aaggtagaag aggccataa aggagagaac accagcttgt tacaccctgt gagcctgcag 3060
ggaatggatg accctgagag agaagtgtta gactggaggt ttgacagccg cctagcattt 3120
catcacgtgg cccgagagct gcatccggag tacttcaaga actgcactag tgagccagta 3180
gatcctagac tagagccctg gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat 3240
tgctattgta aaaagtgttg ctttcattgc caagtttgtt tcataacagc tgccttaggc 3300
atctcctatg gcaggaagaa gcggagacac cgacgaagac ctctcaagg cagtcagact 3360
catcaagttt ctctatcaaa gcaaccacac tccaatcca aaggggagcc gacaggccc 3420
aaggaataa 3429

```

<210> 69

<211> 1142

<212> PRT

<213> Artificial sequence

<220>

<223> HIV-1 ds-gp120c p17/24 Nef Tatm fusion

<400> 69

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10      15
Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65      70      75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100     105     110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115     120     125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130     135     140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145     150     155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165     170     175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180     185     190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195     200     205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210     215     220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225     230     235
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245     250     255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260     265     270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275     280     285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290     295     300

```

## seqlist.txt

```

Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305 310 315 320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325 330 335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340 345 350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
355 360 365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Thr Glu Gly
370 375 380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
385 390 395 400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
405 410 415
Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
420 425 430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
435 440 445
Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
450 455 460
Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
465 470 475 480
Arg Arg Val Val Gln Arg Met Gly Ala Arg Ala Ser Val Leu Ser Gly
485 490 495
Gly Glu Leu Asp Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys
500 505 510
Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu
515 520 525
Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg
530 535 540
Gln Ile Leu Gly Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu
545 550 555 560
Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln
565 570 575
Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu
580 585 590
Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln Ala Ala Asp Thr
595 600 605
Gly His Ser Asn Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile
610 615 620
Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala
625 630 635 640
Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro
645 650 655
Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr
660 665 670
Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys
675 680 685
Glu Thr Ile Asn Glu Glu Ala Glu Trp Asp Arg Val His Pro Val
690 695 700
His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
705 710 715 720
Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
725 730 735
Thr Asn Asn Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
740 745 750
Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
755 760 765
Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770 775 780
Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785 790 795 800
Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
805 810 815
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
820 825 830
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835 840 845

```

seqlist.txt

Leu	Met	Gly	Gly	Lys	Trp	Ser	Lys	Ser	Ser	Val	Val	Gly	Trp	Pro	Thr
850						855					860				
Val	Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala	Asp	Gly	Val	Gly
865					870					875					880
Ala	Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Ser	Asn
				885					890					895	
Thr	Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu	Glu
			900					905					910		
Glu	Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met
		915					920					925			
Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly
	930					935					940				
Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp
945				950						955					960
Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr
				965					970					975	
Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr
			980					985					990		
Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly
	995						1000					1005			
Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp
	1010					1015					1020				
Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe
1025					1030					1035					1040
His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	Thr
			1045						1050					1055	
Ser	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser
			1060					1065					1070		
Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe
		1075					1080					1085			
His	Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	Leu	Gly	Ile	Ser	Tyr	Gly
	1090					1095					1100				
Arg	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr	
1105					1110				1115					1120	
His	Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Lys	Gly	Glu
				1125					1130					1135	
Pro	Thr	Gly	Pro	Lys	Glu										
			1140												

<210> 70  
 <211> 3426  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 mNef Tatm fusion

<400> 70

atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaag	gcctacgaca	cggaagtgc	taacgtgtgg	120
gcgacgcatt	cttgctgtcc	tacggacccc	aacccccagg	aggtggtgct	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtcctt	gaagccctgc	gtgaagctga	cgcctctctg	cgtgacactg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcggg	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaatacgc	gctgttttat	aatctcgatg	tgggtcccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgcccgat	tcgcgaccc	caagtgtaac	aacaagacct	tcgacgggaa	gggcctgtgc	660
accaacgtca	gcacggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	cacccagctg	720
ctgctgaacg	ggtccctggc	tgaggaggag	gtggtgatcc	ggtcggacaa	cttcattggg	780
aacaccaaga	caatcatcgt	ccagctgaac	gagtcgtgtg	cgattaactg	tacccggcct	840
aacaacaaca	cccgtaaagg	catccacatc	gggccttgac	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccat	tgcaacctct	cccgcgcccc	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcagagtt	ctggcgggag	ccccgagatc	gtgcggcact	ccttcaactg	cgggggcgag	1080
ttcttctact	gcgatacgac	acagctcttc	aactccacct	ggaacggcac	cgaggggcaac	1140

seqlist.txt

```

aacacagagg gaaactccac tatcacccctc ccttgccgca tcaagcagat catcaacatg 1200
tgccagaggagg tgggaaaggc catgtatgcc ccccccatcg ggggccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gccggcgggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaagggtggt gaagggtggag ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgtcg tgcagagaat gggtgcccga gcttcggtac tgtctggtgg agagctggac 1500
agatggggaga aaattaggct gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560
gtgtgggcct cgagggagct tgaacggttt gccgtgaacc caggcctgct ggaaacatct 1620
gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680
ctgaggctct tgtataacac agtggctacc ctctactgcg tacaccagag gatcgagatt 1740
aaggatacca agggagcctt ggacaaaatt gaggaggagc aaaacaagag caagaagaag 1800
gcccagcagg cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860
gtccaaaaaca ttcaggggca gatggttcac caggccatca gccccggac gctcaatgcc 1920
tgggtgaagg ttgtcgaaga gaaggccttt tctcctgagg ttatcccat gttctccgct 1980
ttgagtgaagg gggccactcc tcaggacctc aatacaatgc ttaataccgt gggcggccat 2040
caggccgcca tgcaaatgtt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100
gtgcatcccg tccacgctgg cccaatcgcg cccggacaga tgcgggagcc tcgcggtctt 2160
gacattgccc gcaccacctc tacactgcaa gatggatgac caacaatcct 2220
cccattcccg ttggagaaat ctataaacgg tggatcattc tcggtctcaa taaaattgtt 2280
agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340
gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggaggtcaa 2400
aactggatga cggagacact cctggtacag aacgctaacc ccgactgcaa aacaatcttg 2460
aaggcactag gccggctgc caccctggaa gagatgatga ccgctgtca gggagtggc 2520
ggaccgggac acaaagccag agtgttgatg ggcaagtggc caaaaagtag tgtggttgg 2580
tggcctactg taagggaag aatgagacga gctgagccag cagcagatgg ggtgggagca 2640
gcatctcgag acctggaaaa acatggagca atcacaagta gcaatacagc agctaccaat 2700
gctgcttggt cctggctaga agcacaagag gaggaggagg tgggttttcc agtcacacct 2760
caggtacctt taagaccaat gacttacaag gcagctgtag atcttagcca ctttttaaaa 2820
gaaaaggggg gactggaagg gctaattcac tccaacgaa gacaagatat ccttgatctg 2880
tggatctacc acacacaagg ctacttcctt gattggcaga actacacacc agggccaggg 2940
gtcagatatc cactgacctt tggatggtgc tacaagctag taccagttga gccagataag 3000
gtagaagagg ccaataaagg agagaacacc agcttgttac accctgtgag cctgcattga 3060
atggatgacc ctgagagaga agtgtagag tggaggtttg acagccgctt agcatttcat 3120
cacgtggccc gagagctgca tccggagtac ttcaagaact gcactagtga gccagtagat 3180
cctagactag agccctggaa gcatccagga agtcagccta aaactgcttg taccaattgc 3240
tattgtaaaa agtggtgctt tcattgccaa gtttgtttca taacagctgc cttaggcac 3300
tcctatggca ggaagaagcg gagacagcga ctaagggcag ctcaaggcag tcagactcat 3360
caagtttctc tatcaaagca acccacctcc caatccaaag gggagccgac aggcccgaag 3420
gaataa

```

<210> 71  
 <211> 1141  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 mNef Tatm fusion

```

<400> 71
Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10      15
Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20     25     30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35     40     45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50     55     60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65     70     75     80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85     90     95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100    105    110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115    120    125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130    135    140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp

```

## seqlist.txt

```

145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235      240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Val Gln Leu Asn Glu Ser
260      265
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315      320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340      345      350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
355      360      365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Thr Glu Gly
370      375      380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
385      390      395      400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
405      410      415
Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
420      425      430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
435      440      445
Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
450      455      460
Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
465      470      475      480
Arg Arg Val Val Gln Arg Met Gly Ala Arg Ala Ser Val Leu Ser Gly
485      490      495
Gly Glu Leu Asp Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys
500      505      510
Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu
515      520      525
Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg
530      535      540
Gln Ile Leu Gly Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu
545      550      555      560
Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln
565      570      575
Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu
580      585      590
Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln Ala Ala Asp Thr
595      600      605
Gly His Ser Asn Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile
610      615      620
Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala
625      630      635      640
Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro
645      650      655
Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr
660      665      670
Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys
675      680      685
Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val

```



## seqlist.txt

```

690      695      700
His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
705      710      715
Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
725      730      735
Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
740      745      750
Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
755      760      765
Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770      775      780
Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785      790      795
Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
805      810      815
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
820      825      830
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835      840      845
Leu Met Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val
850      855      860
Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala
865      870      875
Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr
885      890      895
Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu
900      905      910
Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
915      920      925
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
930      935      940
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
945      950      955
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
965      970      975
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
980      985      990
Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
995      1000      1005
Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
1010      1015      1020
Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
1025      1030      1035
His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
1045      1050      1055
Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
1060      1065      1070
Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
1075      1080      1085
Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
1090      1095      1100
Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His
1105      1110      1115
Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro
1125      1130      1135
Thr Gly Pro Lys Glu
1140

```

&lt;210&gt; 72

&lt;211&gt; 3429

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; HIV-1 ds-gp120c p17/24 L1-Nef Tatm fusion

&lt;400&gt; 72

seqlist.txt

```

atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60
accaccctct tctgcgcgag cgacgccaag gcctacgaca cggaagtgcg taacgtgtgg 120
gcgacgcatt cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaacgtg 180
accgagtagt tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtccct gaagccctgc gtgaagctga cgctctctg cgtgacactg 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420
aaggtgcaga aggaatacgc gctgttttat aatctcgtat tgggtcccat cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
gtcatgacgc aggcctgccc caaggtgtcc ttgaaccaa tcccgatcca ttactgtgcc 600
cctgccggat tcgcgatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660
accaacgtca gcacggtgca gtgcacccat ggcacccgcc ccgtcgtgag caccagctg 720
ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
aatcatgagt ctggcggaga ccccgagatc gtgcggcact ccttcaactg cggggcgag 1080
ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggcac 1140
aacacagagg gaaactccac tatcacctc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc cccccatcg ggggccagat ccgctgctcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacagacagg agatcttcag gcccgggcgg gcgcacatga gggataactg gcggagcgag 1380
ctgtacaagt acaaggtggg gaaggtggag ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgtcg tgcagagaat ggtgcccga gcttcggtac tgtctggtgg agagctggac 1500
agatgggaga aaattaggct gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560
gtgtgggcct cgagggagct tgaacggttt gccgtgaacc caggcctgct ggaaacatct 1620
gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680
ctgaggtcct tgtataacac agtggctacc ctctactgcg tacaccagag gatcgagatt 1740
aaggatacca aggaggcctt ggacaaaatt gagggaggagc aaaacaagag caagaagaag 1800
gcccagcagg cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860
gtccaaaaca ttcagggcca gatggttcac caggccatca gccccggag gctcaattgc 1920
tgggtgaagg ttgtcgaaga gaaggccttt tctcctgagg ttatcccat gttctccgct 1980
ttgagtgagg gggccactcc tcaggacctc aatacaatgc ttaataccgt gggcggccat 2040
caggccgcca tgcaaatgtt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100
gtgcattccc tccacgtggt cccaatcgcg cccggacaga tgcgggagcc tcgcggtct 2160
gacattggcg gccaccctc tacactgcaa gatggatgag caacaatcct 2220
cccatccag ttggagaaat ctataaacgg tggatcattc tcggtctcaa taaaattgtt 2280
agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340
gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggaggtcaaa 2400
aactgtagta cggagacact cctggtacag aacgctaacc cgcactgcaa aacaatcttg 2460
aaggcactag gcccggtgc caccctggaa gagatgatga ccgcctgtca gggagtggc 2520
ggacccggac acaaagccag agtgttgatg ggtggcaagt ggtcaaaaag tagtgtggtt 2580
ggatggccta ctgtaaggga aagaatgaga cgagctgagc cagcagcaga tggggtggga 2640
gcagcatctc gagacctgga aaaacatgga gcaatcacia gtagcaatac agcagctacc 2700
aatgctgctt gtgcttggc agaagcacia gaggaggagg aggtgggttt tccagtcaca 2760
cctcaggtac ctttaagacc aatgacttac aaggcagctg tagatcttag ccacttttta 2820
aaagaaaagg ggggactgga agggctaatt cactcccaac gaagacaaga tatccttgat 2880
ctgtggatct accacacaca aggctacttc cctgattggc agaactacac accagggcca 2940
ggggtcagat atccactgac ctttggatgg tgctacaagc tagtaccagt tgagccagat 3000
aaggtagaag aggccaataa accagcgctt tacaccctgt gagcctgcat 3060
ggaatggatg accctgagag agaagtgtta gagtggaggt ttgacagccg cctagcattt 3120
catcacgtgg cccgagagct gcatccggag tacttcaaga actgcactag tgagccagta 3180
gatcctagac tagagccctg gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat 3240
tgctattgta aaaagtgtg ctttcattgc caagtgtgtt tcataacagc tgccttaggc 3300
atctcctatg gcaggaagaa gcggagacag cgacgaagac ctcctcaagg cagtcagact 3360
catcaagttt ctctatcaaa gcaaccacc tccaatcca aaggggagcc gacaggcccc 3420
aaggaataa

```

<210> 73

<211> 1142

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 L1-Nef Tatm fusion

<400> 73

## seqlist.txt

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
 1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
 20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
 35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
 50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
 65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
 85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235      240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315      320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340      345      350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
355      360      365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly
370      375      380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
385      390      395      400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
405      410      415
Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
420      425      430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
435      440      445
Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
450      455      460
Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
465      470      475      480
Arg Arg Val Val Gln Arg Met Gly Ala Arg Ala Ser Val Leu Ser Gly
485      490      495
Gly Glu Leu Asp Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys
500      505      510
Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu
515      520      525
Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg
530      535      540

```

## seqlist.txt

Gln Ile Leu Gly Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu  
 545 550 555 560  
 Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln  
 565 570 575  
 Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu  
 580 585 590  
 Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln Ala Ala Asp Thr  
 595 600 605  
 Gly His Ser Asn Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile  
 610 615 620  
 Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala  
 625 630 635 640  
 Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro  
 645 650 655  
 Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr  
 660 665 670  
 Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys  
 675 680 685  
 Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val  
 690 695 700  
 His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser  
 705 710 715 720  
 Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met  
 725 730 735  
 Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile  
 740 745 750  
 Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile  
 755 760 765  
 Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp  
 770 775 780  
 Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys  
 785 790 795 800  
 Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys  
 805 810 815  
 Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met  
 820 825 830  
 Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val  
 835 840 845  
 Leu Met Gly Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr  
 850 855 860  
 Val Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly  
 865 870 875 880  
 Ala Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn  
 885 890 895  
 Thr Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu  
 900 905 910  
 Glu Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met  
 915 920 925  
 Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly  
 930 935 940  
 Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp  
 945 950 955 960  
 Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr  
 965 970 975  
 Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr  
 980 985 990  
 Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly  
 995 1000 1005  
 Glu Asn Thr Ser Ala Leu His Pro Val Ser Leu His Gly Met Asp Asp  
 1010 1015 1020  
 Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe  
 1025 1030 1035 1040  
 His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr  
 1045 1050 1055  
 Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser  
 1060 1065 1070  
 Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe  
 1075 1080 1085

seqlist.txt

His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly  
 1090 1095 1100  
 Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr  
 1105 1110 1115 1120  
 His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu  
 1125 1130 1135  
 Pro Thr Gly Pro Lys Glu  
 1140

<210> 74  
 <211> 3429  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 L2-Nef Tatm fusion

<400> 74  
 atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60  
 accaccctct tctgcgcgag cgacgccaag gcctacgaca cggaagtgc taacgtgtgg 120  
 gcgagcgtat cttgcgtgcc tacggacccc aacccccagg aggtgggtgt gggaaacgtg 180  
 accgagtact tcaacatgtg gaagaataac atgggtggatc agatgcacga ggacatcatc 240  
 tctctgtggg accagtcctt gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300  
 gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360  
 gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420  
 aaggtgcaga aggaatacgc gctgttttat aatctcgatg tggccccat cgacgacgac 480  
 aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540  
 gtcagtacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600  
 cctgcccgat tcgcatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660  
 accaacgtca gcacgggtga gtgaccccat ggcattccgc ccgtcgtgag caccagctg 720  
 ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780  
 aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840  
 aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgcccgc 900  
 aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960  
 accctgaagc agatcgtgat caagctgaga gacactttg gaaacaagac catcaagttc 1020  
 aatcagagtt ctggcgagga ccccgagatc gtgcggcact ccttcaactg cgggggagcag 1080  
 ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggcaac 1140  
 aacacagagg gaaactccac tatcacctc ccttgccgca tcaagcagat catcaacatg 1200  
 tggcaggagg tgggaaaggc catgtatgcc cccccatcg ggggagcag ccgctgctcc 1260  
 tccaacatca ccggcctgtc gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320  
 aacgagacgg agatcttcag gcccggcgcg ggcgacatga gggataactg gcggagcgag 1380  
 ctgtacaagt acaaggtggg gaaggtggag ccgctcggcg tggccccac ccgggccaag 1440  
 cgccgcgtcg tgcagagaat ggggtgcccga gcttcggtac tgtctgggtg agagctggac 1500  
 agatggggaga aaattaggct gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560  
 gtgtgggccc agaggtagct tgaacgggtt gccgtgaacc caggcctgct ggaaacatct 1620  
 gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680  
 ctgaggtcct tgtataacac agtggctacc ctctactgcg tacaccagag gatcgagatt 1740  
 aaggatacca aggaggcctt ggacaaaatt gaggaggagc aaaacaagag caagaagaag 1800  
 gccagcagg cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860  
 gtccaaaaca ttcagggcca gatggttcat caggccatca gccccggac gctcaatgcc 1920  
 tgggtgaagg ttgtcgaaga gaaggccttt tctcctgagg ttatcccat gttctccgct 1980  
 ttgagtgaagg gggccactcc tcaggacctc aatacaatgc ttaataccgt gggcggccat 2040  
 caggccgcca tgcaaatgtt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100  
 gtgcatcccg tccacgctgg cccaatcgcg cccggacaga tgcgggagcc tcgcggtct 2160  
 gacattgccg gcaccacctc tacttgcaa gagcaatcg gatggatgac caacaatcct 2220  
 cccatcccag ttggagaaat ctataaacgg ttgatcattc tcggtctcaa taaaattgtt 2280  
 agaattgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340  
 gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggagggtcaa 2400  
 aactgtagta cggagacact cctggtacag aacgctaacc ccgactgcaa aacaatcttg 2460  
 aaggcactag gcccggctgc caccctggaa gagatgatga ccgctgtca gggagtaggc 2520  
 ggacccggac acaaagccag agtgttgatg ggtggcaagt ggtcaaaaag tagtgtggtt 2580  
 ggatggccta ctgtaaggga aagaatgaga cgagctgagc cagcagcaga tggggtggga 2640  
 gcagcatctc gagactgga aaaacatgga gcaatcaca gtagaatac agcagctacc 2700  
 aatgctgctt gtgcctggct agaagcaca aggtgggttt tccagtcaca 2760  
 cctcaggtac cttaagacc aatgacttac aaggcagctg tagatcttag ccacttttta 2820  
 aaagaaaagg ggggactgga agggctaatt cactcccaac gaagacaaga tatccttgat 2880  
 ctgtggatct accacacaca aggtacttcc cctgattggc agaactacac accagggcca 2940

seqlist.txt

```

gggggtcagat atccactgac ctttggatgg tgctacaagc tagtaccagt tgagccagat 3000
aaggtagaag aggccaataa aggagagaac accagcttgg cacaccctgt gagcctgcat 3060
ggaatggatg accctgagag agaagtgtta gagtggaggt ttgacagccg cctagcattt 3120
catcacgtgg cccgagagct gcatccggag tacttcaaga actgcactag tgagccagta 3180
gatcctagac tagagccctg gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat 3240
tgctattgta aaaagtgttg ctttcattgc caagtttgtt tcataacagc tgccttaggc 3300
atctcctatg gcaggaagaa gcgagagacag cgacgaagac ctcctcaagg cagtcagact 3360
catcaagttt ctctatcaaa gcaacccacc tcccaatcca aaggggagcc gacaggcccg 3420
aaggaataa

```

<210> 75

<211> 1142

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 L2-Nef Tatm fusion

<400> 75

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
 1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
 20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
 35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
 50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
 65      70      75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
 85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser
260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
340      345      350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
355      360      365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly
370      375      380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met

```

## seqlist.txt

```

385      390      395      400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
405 Ser Asn Ile Thr Gly 410 Leu Leu Leu Thr Arg 415 Asp Gly
Ile Arg Cys Ser 420 Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
435 Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu 445 Leu Tyr Lys Tyr
450 Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
465 Arg Arg Val Val Gln Arg Met Gly Ala Arg Ala Ser Val Leu Ser 480 Gly
485 Gly Glu Leu Asp Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys
500 Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg 510 Glu Leu Glu
515 Arg Phe Ala Val Asn Pro Gly 520 Leu Leu Glu Thr Ser 525 Gly Cys Arg
530 Gln Ile Leu Gly Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu
545 Leu Arg Ser Leu Tyr 550 Asn Thr Val Ala Thr 555 Leu Tyr Cys Val His 560 Gln
565 Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu
580 Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln Ala Ala Asp Thr
595 Gly His Ser Asn Gln Val Ser 600 Gln Asn Tyr Pro Ile Val Gln Asn Ile
610 Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala
625 Trp Val Lys Val Val Glu Glu Lys Ala Phe 635 Ser Pro Glu Val Ile 640 Pro
645 Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr
660 Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys
675 Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val
690 His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
705 Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
725 Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
740 Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
755 Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770 Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785 Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
805 Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Met
820 Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835 Leu Met Gly Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr
850 Val Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly
865 Ala Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn
885 Thr Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu
900 Glu Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met
915 Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly

```

seqlist.txt

```

      930                      935                      940
Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp
945
Leu Trp Ile Tyr His 950 Gln Gly Tyr Phe 955 Asp Trp Gln Asn Tyr
960
Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr
975
Lys Leu Val 980 Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly
990
Glu Asn Thr Ser Leu Ala His Pro Val Ser Leu His Gly Met Asp Asp
1000
Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe
1005
1010
1015
1020
1025
His His Val Ala Arg 1030 Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr
1035
1040
1045
1050
1055
Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
1060
1065
1070
Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
1075
1080
1085
His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly
1090
1095
1100
Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
1105
1110
1115
His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu
1120
1125
1130
1135
Pro Thr Gly Pro Lys Glu
1140

```

<210> 76  
 <211> 3429  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 LL-Nef Tatm fusion

```

<400> 76
atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60
accacccctct tctgcgcgag cgacgccaaag gcctacgaca cggaagtgca taacgtgtgg 120
gcgacgcattg cttgcgtgcc tacggacccc aacccccagg aggtgggtgct gggaaacgtg 180
accgagtact tcaacatgtg gaagaataac atgggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtcctt gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420
aaggtgcaga aggaatacgc gctgttttat aatctcgtat tggtcccat cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
gtcatgacgc aggcctgccc caagggtgcc ttcgaaccaa tcccgatcca ttactgtgcc 600
cctgccggat tcgcgatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660
accaacgtca gcacggtgca gtgcacccat ggcatccgcc ccgtcgtgag caccagctg 720
ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgcccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcca gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
aatcagagtt ctggcggaga ccccgagatc gtgcggcact ccttcaactg cgggggagc 1080
ttcttctact gcgatacgac acagctcttc aactccacct ggaacggcac cgagggaac 1140
aacacagagg gaaactccac tatcaccttc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc cccccatcg ggggcccagat ccgctgtcc 1260
tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcag 1380
ctgtacaagt acaaggtggg gaagggtggg ccgctcggcg tggccccac ccgggccaag 1440
cgccgcgtcg tgcagagaat ggggtgccga gcttcggtac tgtctgggtg agagctggag 1500
agatgggaga aaatttaggt gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560
gtgtgggcct agaggagct tgaacggttt gccgtgaacc caggcctgct ggaaacatct 1620
gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680
ctgaggtcct tgtataacac agtggctacc ctctactgcg tacaccagag gatcgagatt 1740
aaggatacca aggaggcctt ggacaaaatt gaggaggagc aaaacaagag caagaagaag 1800

```



seqlist.txt

```

gcccagcagg cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860
gtccaaaaca ttccaggcca gatgggtcat caggccatca gcccccgac gctcaatgcc 1920
tgggtgaagg ttgtcgaaga gaaggccttt tctcctgagg ttatccccat gttctccgct 1980
ttgagtgaagg gggccactcc tcaggacctc aatacaatgc ttaataccgt gggcgcccat 2040
cagggcgcca tgcaaatggt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100
gtgcatcccg tccacgctgg cccaatcgcg cccggacaga tgcgggagcc tcgcggtctt 2160
gacattgccg gcaccacctc tacactgcaa gagcaaatcg gatggatgac caacaatcct 2220
cccattccag ttggagaaat ctataaacgg tggatcattc tcggtctcaa taaaattggt 2280
agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340
gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggaggtcaaa 2400
aactggatga cggagacact cctggtacag aacgctaacc ccgactgcaa aacaatcttg 2460
aaggcactag gccccggctgc caccctggaa gagatgatga ccgcctgtca gggagtaggc 2520
ggacccggac acaaagccag agtggtgatg ggtggcaagt ggtcaaaaag tagtgtggtt 2580
ggatggccta ctgtaaggga aagaatgaga cgagctgagc cagcagcaga tggggtgga 2640
gcagcatctc gagacctgga aaaacatgga gcaatcacia gtagcaatac agcagctacc 2700
aatgctgctt gtgcctggct agaagcacia gaggaggagg aggtgggttt tccagtcaca 2760
cctcaggtac ctttaagacc aatgacttac aaggcagctg tagatcttag ccacttttta 2820
aaagaaaagg ggggactgga agggctaatt cactccaac tatccttgat 2880
ctgtggatct accacacaca aggcctactc cctgattggc agaactacac accagggcca 2940
ggggctcagat atccactgac ctttggatgg tgctacaagc tagtaccagt tgagccagat 3000
aaggtagaag aggccaataa aggagagaac accagcgccg cacaccctgt gagcctgcat 3060
ggaatggatg accctgagag agaagtgtta gagtggaggt ttgacagccg cctagcattt 3120
catcactgtg cccgagagct gcattccggag tacttcaaga actgcactag tgagccagta 3180
gatcctagac tagagccctg gaagcatcca ggaagtcagc ctaaaactgc ttgtaccaat 3240
tgctattgta aaaagtgttg ctttcattgc caagtttggt tcataacagc tgccttaggc 3300
atctcctatg gcaggaagaa gcggagacag cgacgaagac ctcctcaagg cagtcagact 3360
catcaagttt ctctatcaaa gcaaccacc tcccaatcca aaggggagcc gacaggcccc 3420
aaggaataa

```

<210> 77

<211> 1142

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 LL-Nef Tatm fusion

<400> 77

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65      70      75
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
100     105     110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
115     120     125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
130     135     140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145     150     155
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
165     170     175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
180     185     190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
195     200     205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210     215     220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225     230     235     240

```

seqlist.txt

Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp
				245					250					255	
Asn	Phe	Met	Asp	Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser
			260					265					270		
Val	Ala	Ile	Asn	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile
		275					280					285			
His	Ile	Gly	Pro	Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly
	290					295					300				
Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn
	305				310					315				320	
Thr	Leu	Lys	Gln	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys
			325						330					335	
Thr	Ile	Lys	Phe	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg
			340					345					350		
His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln
		355					360					365			
Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly
	370					375					380				
Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn	Met
	385				390					395				400	
Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln
			405						410					415	
Ile	Arg	Cys	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	
			420				425					430			
Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro
		435					440					445			
Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr
	450					455					460				
Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys
	465				470					475				480	
Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly
			485						490					495	
Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys
			500					505					510		
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu
		515					520					525			
Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg
	530					535					540				
Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu
	545				550					555				560	
Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln
			565					570						575	
Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu
			580					585					590		
Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr
		595					600					605			
Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile
	610					615					620				
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala
	625				630					635				640	
Trp	Val	Lys	Val	Val	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	
			645					650					655		
Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr
			660					665					670		
Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys
		675					680					685			
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val
	690					695					700				
His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser
	705				710					715				720	
Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met
			725						730					735	
Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile
			740					745					750		
Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile
		755					760					765			
Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp
	770					775					780				

seqlist.txt

```

Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785 790 795 800
Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
805 810 815
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
820 825 830
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835 840 845
Leu Met Gly Gly Lys Trp Ser Ser Ser Val Val Gly Trp Pro Thr
850 855 860
Val Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly
865 870 875 880
Ala Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn
885 890 895
Thr Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu
900 905 910
Glu Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met
915 920 925
Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly
930 935 940
Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp
945 950 955 960
Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr
965 970 975
Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr
980 985 990
Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly
995 1000 1005
Glu Asn Thr Ser Ala Ala His Pro Val Ser Leu His Gly Met Asp Asp
1010 1015 1020
Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe
1025 1030 1035 1040
His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr
1045 1050 1055
Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
1060 1065 1070
Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
1075 1080 1085
His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly
1090 1095 1100
Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
1105 1110 1115 1120
His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu
1125 1130 1135
Pro Thr Gly Pro Lys Glu
1140

```

<210> 78

<211> 3426

<212> DNA

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 mLL-Nef Tatm fusion

<400> 78

```

atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60
accaccctct tctgcgcgag cgacgccaag gcctacgaca cggaagtgca taactgtgtg 120
gcgacgcgatg cttgcgtgcc tacggacccc aacccccagg aggtgggtgct gggaaacgtg 180
accgagtact tcaacatgtg gaagaataac atgggtggatc agatgcacga ggacatcatc 240
tctctgtggg accagtcctt gaagccctgc gtgaagctga cgcctctctg cgtgacactg 300
gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360
gagattcgga agggcgagat caagaactgc tcttcaata tcacgacctc gatcagagac 420
aaggtgcaga aggaatacgc gctgttttat aatctcgatg tgggtcccat cgacgacgac 480
aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540
gtcatgacgc aggcctgccc caagggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600
cctgccggat tcgcgatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660

```

# seqlist.txt

```

accaaagtcg gacaggtgca gtgcacccat ggcattccgc ccgtcgtgag caccagctg 720
ctgctgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780
aacaccaaga caatcatcgt ccagctgaac gagtctgtgg cgattaactg taccggcct 840
aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccggccgc 900
aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcccc gtggaataac 960
accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020
aatcagagtt ctggcgagga ccccgagatc gtgcggcact cttcaactg cgggggag 1080
ttcttctact gcgatagcac acagctcttc aactccacct ggaacggcac cgagggaac 1140
aacacagagg gaaactccac tatcaccctc ccttgccgca tcaagcagat catcaacatg 1200
tggcaggagg tgggaaaggc catgtatgcc ccccccacgc ggggcccagat ccgctgctcc 1260
tccaacatca cgggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320
aacgagacgg agatcttcag gcccgccggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaagggtgt gaaggtggag ccgctcggcg tggccccac cggggccaag 1440
cgccgcgtcg tgcagagaat ggtgcccga ctcteggtac tgtctggtgg agagctggag 1500
agatgggaga aaattaggct gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560
gtgtgggcct cgagggagct tgaacggttt gccgtgaacc caggcctgct ggaaacatct 1620
gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gagtgaagag 1680
ctgaggtact agtggctacc agtactgcg tacaccagag gatcgagatt 1740
aagataacca aggaggcctt ggacaaaatt gaggaggagc aaaaacagag caagaagaag 1800
gcccagcagg cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860
gtccaaaaca ttcaggggca gatggttcat caggccatca gcccccgac gctcaatgcc 1920
tgggtgaagg ttgtcgaaga gaaggccttt tctctgagg ttatcccat gttctccgct 1980
ttgagttagg gggccactcc tcaggacctc aatacaatgc ttaataccgt gggcgccat 2040
caggccgcca tgcaaatgtt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100
gtgcatcccg tccacgctgg cccaatcgcg cccggacaga tgcgggagcc tcgcggtct 2160
gacattgccg gcaccacctc tacactgcaa gagcaaatcg gatggatgac caacaatcct 2220
cccattccag ttggagaaat ctataaacgg ttgatcattc tcggtctcaa taaaattggt 2280
agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340
gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggaggtcaa 2400
aactggatga cggagacact cctggtacag aacgctaacc ccgactgcaa aacaatcctg 2460
aaggcactag gcccggctgc caccctggaa gagatgatga ccgcctgtca gggagtaggc 2520
ggaccggagc acaaagccag agtgttgatg ggcaagtggg caaaaagtag tgtggttgg 2580
tggcctactg taagggaagg aatgagacga gctgagccag cagcagatgg ggtgggagca 2640
gcatctcgag acctggaaaa acatggagca atcacaagta gcaatacagc agctaccaat 2700
gctgcttgtg cctggctaga agcacaagag gaggaggagg tgggttttcc agtcacacct 2760
caggtacctt taagaccaat gacttacaag gcagctgtag atcttagcca ctttttaaaa 2820
gaaaaggggg gactggaagg gctaattcac tccaacgaa gacaagatat ccttgatctg 2880
tggatctacc acacacaagg ctacttcctt gattggcaga actacacacc agggccaggg 2940
gtcagatata cactgacctt tggatggtgc tacaagctag taccagttga gccagataag 3000
gtagaagagg ccaataaagg agagaacacc agcgccgcac accctgtgag cctgcatgga 3060
atggatgacc ctgagagaga agtgttagag tggagtttg acagccgctc agcattttc 3120
cacgtggccc gagagctgca tccggagtac ttcaagaact gcactagtga gccagtagat 3180
cctagactag agccctggaa gcatccagga agtcagccta aaactgcttg taccaattgc 3240
tattgtaaaa agtgttgctt tcattgccaa gtttgtttca taacagctgc cttaggcata 3300
tcctatggca ggaagaagcg gagacagcga cgaagacctc ctcaaggcag tcagactcat 3360
caagtttctc tatcaaagca acccacctcc caatccaaag gggagccgac aggcccaag 3420
gaataa

```

<210> 79

<211> 1141

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 mLL-Nef Tatm fusion

<400> 79

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10      15
Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
20     25     30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
35     40     45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
50     55     60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65     70     75     80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu

```

90

Page 45

## seqlist.txt

```

625      630      635      640
Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro
645      650      655
Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr
660      665      670
Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys
675      680      685
Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val
690      695      700
His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
705      710      715      720
Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
725      730      735
Thr Asn Asn Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
740      745      750
Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
755      760      765
Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
770      775      780
Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
785      790      795      800
Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
805      810      815
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
820      825      830
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
835      840      845
Leu Met Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val
850      855      860
Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala
865      870      875      880
Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr
885      890      895
Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu
900      905      910
Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
915      920      925
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
930      935      940
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
945      950      955      960
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
965      970      975
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
980      985      990
Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
995      1000      1005
Asn Thr Ser Ala Ala His Pro Val Ser Leu His Gly Met Asp Asp Pro
1010      1015      1020
Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
1025      1030      1035      1040
His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
1045      1050      1055
Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
1060      1065      1070
Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
1075      1080      1085
Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
1090      1095      1100
Lys Lys Arg Arg Gln Arg Arg Pro Pro Gln Gly Ser Gln Thr His
1105      1110      1115      1120
Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro
1125      1130      1135
Thr Gly Pro Lys Glu
1140

```

## seqlist.txt

<211> 3426  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 mL1-Nef Tatm fusion

<400> 80

atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaag	gcctacgaca	cggaagtgc	taacgtgtgg	120
gcgacgcatg	cttgctgtcc	tacggacccc	aacccccagg	aggtggtgct	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtccct	gaagccctgc	gtgaagctga	cgcttctctg	cgtgacactg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaatacgc	gctgttttat	aatctcgatg	tgggtcccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgcgt	aatttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	agggctgtcc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgcccggat	tcgcatcctt	caagtgtaac	aacaagacct	tcgacgggaa	gggctgtgtc	660
accaacgtca	gcacggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	caccagctgt	720
ctgctgaacg	gggtccctggc	tgaggaggag	gtggtgatcc	ggtcggacaa	cttcatggac	780
aacaccaaga	caatcatcgt	ccagctgaac	gagtcgtgtg	cgattaactg	taccggcctc	840
aacaacaaga	cccgtaaagg	catccacatc	gggccttgag	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccat	tgcaacctct	cccgcgcca	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcagagtt	ctggcggaga	ccccgagatc	gtgcggcact	ccttcaactg	cgggggcgag	1080
ttcttctact	gcgatacgac	acagctcttc	aactccacct	ggaacggcac	cgagggcaac	1140
aacacagagg	gaaactccac	tatcacccct	ccttgccgca	tcaagcagat	catcaacatg	1200
tggcaggagg	tgggaaaggc	catgtatgcc	cccccatcg	ggggccagat	ccgctgtctc	1260
tccaacatca	ccggcctgct	gctcaccaga	gacgggggca	ccgagggcaa	cggcacggag	1320
aacgagacgg	agatcttcag	gcccggcggc	ggcgacatga	gggataactg	gcggagcgag	1380
ctgtacaagt	acaaggtggg	gaaggtggag	ccgtctggcg	tggcccccac	ccgggccaag	1440
cgccgcgtcg	tgcagagaat	gggtgccgga	gcttcggtac	tgtctggtgg	agagctggac	1500
agatgggaga	aaattaggct	gcgcccggga	ggcaaaaaga	aatacaagct	caagcatatc	1560
gtgtgggcct	cgagggagct	tgaacggttt	gccgtgaacc	caggcctgct	ggaaacatct	1620
gagggatgtc	gccagatcct	ggggcaattg	cagccatccc	tccagaccgg	gagtgaagag	1680
ctgaggtcct	tgtataacac	agtggctacc	ctctactcg	tacaccagag	gattcgagatt	1740
aaggatacca	aggaggcctt	ggacaaaatt	gaggaggagc	aaaacaagag	caagaagaag	1800
gcccagcagg	cagctgtctga	cactgggcat	agcaaccagg	tatcacagaa	ctatcctatt	1860
gtccaaaaca	ttcaggggcca	gatggttcat	caggccatca	gcccccgac	gctcaatgcc	1920
tgggtgaagg	ttgtcgaaga	gaaggccttt	ttctctgagg	ttatccccat	gttctccgct	1980
ttgagtgaag	gggccactcc	tcaggacctc	aatacaatgc	ttaataccgt	gggcggccat	2040
caggccgcca	tgcaaatgtt	gaaggagact	atcaacgagg	aggcagccga	gtgggacaga	2100
gtgcatcccg	tccacgctgg	cccaatcgcg	cccggacaga	tgccggagcc	tcgctgctct	2160
gacattgccg	gcaccacctc	tacactgcaa	gagcaaatcg	gatggatgac	caacaatcct	2220
cccattccag	ttggagaat	ctataaacgg	tggatcattc	tcggtctcaa	taaaattgtt	2280
agaatgtact	ctccgacatc	catccttgac	attagacagg	gacccaaaga	gccttttagg	2340
gattacgtcg	accggtttta	taagaccctg	cgagcagagc	aggcctctca	ggaggtcaaa	2400
aactggatga	cggagacact	cctggtacag	aacgctaacc	ccgactgcaa	aacaatcttg	2460
aaggcactag	gcccggctgc	caccctggaa	gagatgatga	ccgcctgtca	gggagtaggc	2520
ggaccgggac	acaaagccag	agtgttgatg	ggcaagtggg	caaaaagtag	tgtggttgga	2580
tggcctactg	taagggaag	aatgagacga	gctgagccag	cagcagatgg	ggtgggagca	2640
gcatctcgag	acctggaaaa	acatggagca	atcacaaagta	gcaatacagc	agctaccaat	2700
gctgcttggt	cctggctaga	agcacaagag	gaggaggagg	tgggttttcc	agtcacacct	2760
caggtacctt	taagaccaat	gacttacaag	gcagctgtag	atcttagcca	ctttttaaaa	2820
gaaaaggggg	gactggaagg	gctaattcac	tccaacgaa	gacaagatat	ccttgatctg	2880
tggatctacc	acacacaagg	ctacttcctt	gattggcaga	actacacacc	agggccaggg	2940
gtcagatatc	cactgacctt	tggatggtgc	tacaagctag	taccagttga	gccagataag	3000
gtagaagagg	ccaataaagg	agagaacacc	agcgccttac	accctgtgag	cctgcatgga	3060
atggatgacc	ctgagagaga	agtgttagag	tggaggtttg	acagccgcct	agcatttcac	3120
cacgtggccc	gagagctgca	tccggagtac	ttcaagaact	gcactagtga	gccagtagat	3180
cctagactag	agccctggaa	gcatccagga	agtcagccta	aaactgcttg	taccaattgc	3240
tattgtaaaa	agtgttgctt	tcattgccaa	gtttgtttca	taacagctgc	cttaggcac	3300
tcctatggca	ggaagaagcg	gagacagcga	cgaagacctc	ctcaaggcag	tcagactcat	3360
caagtttctc	tatcaaagca	acccacctcc	caatccaaag	gggagccgac	aggcccgaag	3420
gaataa						3426

<210> 81

## seqlist.txt

&lt;211&gt; 1141

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; HIV-1 ds-gp120c p17/24 mL1-Nef Tatm fusion

&lt;400&gt; 81

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
1      5      10      15
Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
      20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
      35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
      50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
      85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
      100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
      115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
      130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
      165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
      180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
      195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
225      230      235      240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
      245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Val Gln Leu Asn Glu Ser
      260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
      275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
305      310      315      320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys
      325      330      335
Thr Ile Lys Phe Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg
      340      345      350
His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln
      355      360      365
Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly
370      375      380
Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met
385      390      395      400
Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln
      405      410      415
Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly
      420      425      430
Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro
      435      440      445
Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr
450      455      460
Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys
465      470      475      480

```



## seqlist.txt

Arg	Arg	Val	Val	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly
				485					490					495	
Gly	Glu	Leu	Asp	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys
			500					505					510		
Lys	Lys	Tyr	Lys	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu
		515					520					525			
Arg	Phe	Ala	Val	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg
	530					535					540				
Gln	Ile	Leu	Gly	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu
545					550					555					560
Leu	Arg	Ser	Leu	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln
				565					570					575	
Arg	Ile	Glu	Ile	Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu
			580					585					590		
Glu	Gln	Asn	Lys	Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr
		595					600					605			
Gly	His	Ser	Asn	Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile
	610					615					620				
Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala
625					630					635					640
Trp	Val	Lys	Val	Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro
				645					650					655	
Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr
			660					665					670		
Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys
		675					680					685			
Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val
	690					695					700				
His	Ala	Gly	Pro	Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser
705					710					715					720
Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met
				725					730					735	
Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile
			740					745					750		
Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile
		755					760					765			
Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp
	770					775					780				
Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys
785					790					795					800
Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys
				805					810					815	
Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met
			820					825					830		
Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val
		835					840					845			
Leu	Met	Gly	Lys	Trp	Ser	Lys	Ser	Ser	Val	Val	Gly	Trp	Pro	Thr	Val
	850					855					860				
Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala	Asp	Gly	Val	Gly	Ala
865					870				875						880
Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Ser	Asn	Thr
				885					890					895	
Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu	Glu	Glu
			900					905					910		
Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met	Thr
		915					920					925			
Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly
	930					935					940				
Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp	Leu
945					950					955					960
Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
				965					970					975	
Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys
			980					985					990		
Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly	Glu
		995					1000					1005			
Asn	Thr	Ser	Ala	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro
	1010					1015					1020				

seqlist.txt

Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His  
 1025 1030 1035 1040  
 His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser  
 1045 1050 1055  
 Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln  
 1060 1065 1070  
 Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His  
 1075 1080 1085  
 Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg  
 1090 1095 1100  
 Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His  
 1105 1110 1115 1120  
 Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro  
 1125 1130 1135  
 Thr Gly Pro Lys Glu  
 1140

<210> 82  
 <211> 3426  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c p17/24 mL2-Nef Tatm fusion

<400> 82  
 atggccgagc agctgtgggt caccgtctac tacggcgtgc ctgtgtggaa ggaggccacg 60  
 accaccctct tctgcgcgag cgacgccaag gcctacgaca cggaagtgc taactgtgtg 120  
 gcgacgcatg cttgcgtgcc tacggacccc aacccccagg aggtggtgct gggaaaacgtg 180  
 accgagtact tcaacatgtg gaagaataac atggtggatc agatgcacga ggacatcatc 240  
 tctctgtggg accagtcctt gaagccctgc gtgaagctga cgctctctg cgtgacactg 300  
 gactgtgacg acgtcaacac caccaacagc actaccacca ccagcaacgg ctggaccgga 360  
 gagattcgga agggcgagat caagaactgc tccttcaata tcacgacctc gatcagagac 420  
 aaggtgcaga aggaatacgc gctgttttat aatctcgatg tgggtccccat cgacgacgac 480  
 aatgccacca ccaagaacaa gacgacgcgt aatttcagac tcattcactg caacagcagc 540  
 gtcatgacgc aggcctgccc caaggtgtcc ttcgaaccaa tcccgatcca ttactgtgcc 600  
 cctgcccgat tcgcgatcct caagtgtaac aacaagacct tcgacgggaa gggcctgtgc 660  
 accaacgtca gcacggtgca gtgcacccat ggcattccgc ccgtcgtgag caccacagctg 720  
 ctgtgaacg ggtccctggc tgaggaggag gtggtgatcc ggtcggacaa cttcatggac 780  
 aacaccaaga caatcatcgt ccagctgagc gactctgtgg cgattaactg taccggcctc 840  
 aacaacaaca cccgtaaggg catccacatc gggcctggac gggccttcta tgccgcccgc 900  
 aagatcatcg gcgacatccg gcaggcccat tgcaacctct cccgcgcccc gtggaataac 960  
 accctgaagc agatcgtgat caagctgaga gagcactttg gaaacaagac catcaagttc 1020  
 aatcagagtt ctggcggaga ccccgagatc gtgcggcact ctttcaactg cgggggacag 1080  
 ttcttctact cgtatacgac acagctcttc aactccacct ggaacggcac cgagggcaac 1140  
 aacacagagg gaaactccac tatcaccttc ccttgccgca tcaagcagat catcaacatg 1200  
 tggcaggagg tgggaaaggc catgtatgcc ccccccacgc ggggccagat ccgctgctcc 1260  
 tccaacatca ccggcctgct gctcaccaga gacgggggca ccgagggcaa cggcacggag 1320  
 aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgaag 1380  
 ctgtacaagt acaaggtggg gaaggtggag ccgctcggcg tggccccac ccgggccaag 1440  
 cgccgcgtcg tgcagagaat ggggtgccga gcttcggtac tgtctggtgg agagctggac 1500  
 agatgggaga aaattaggct gcgcccggga ggcaaaaaga aatacaagct caagcatatc 1560  
 gtgtgggcct cgagggagct tgaacggttt gccgtgaacc caggcctgct ggaaacatct 1620  
 gagggatgtc gccagatcct ggggcaattg cagccatccc tccagaccgg gactgaagag 1680  
 ctgaggtcct tgtataacac agtggctacc ctctactgcg tacaccagag gatcgagatt 1740  
 aaggatacca aggaggcctt ggacaaaatt gaggaggagc aaaacaagag caagaagaag 1800  
 gccagcagg cagctgctga cactgggcat agcaaccagg tatcacagaa ctatcctatt 1860  
 gtccaaaaa ttcagggcca gatggttcat caggccatca gccccggac gctcaatgcc 1920  
 tgggtgaagg ttgtcgaaag gaagtccttt tctctgagg ttatccccat gttctccgct 1980  
 ttgagtgaag gggccactcc tcaggacctc aatacaatgc ttaataccgt gggcggccat 2040  
 caggccgcca tgcaaatgtt gaaggagact atcaacgagg aggcagccga gtgggacaga 2100  
 gtgcatcccc tccacgttgg cccaatcgcg cccggacaga tgcgggagcc tcgcggtctc 2160  
 gacattgccg gcaccacctc tacactgcaa gatggatgac caacaatcct 2220  
 cccatccagg ttggagaaat ctataaacgg tggatcattc tcggtctcaa taaaattgtt 2280  
 agaatgtact ctccgacatc catccttgac attagacagg gacccaaaga gccttttagg 2340  
 gattacgtcg accggtttta taagaccctg cgagcagagc aggcctctca ggagggtcaaa 2400  
 aactggatga cggagacact cctggtacag aacgctaacc ccgactgcaa aacaatcttg 2460

seqlist.txt

```

aaggcactag gcccggctgc caccctggaa gagatgatga ccgcctgtca gggagtaggc 2520
ggaccccgac acaaagccag agtggtgatg ggcaagtggg caaaaagtag tgtgggttga 2580
tgccctactg taagggaaaag aatgagacga gctgagccag cagcagatgg ggtgggagca 2640
gcattctcag acctggaaaa acatggagca atcacaagta gcaatacagc agctaccaat 2700
gctgcttgtg cctggctaga agcacaagag gaggaggagg tgggttttcc agtcacacct 2760
caggtacctt taagaccaat gacttacaag gcagctgtag atcttagcca ctttttaaaa 2820
gaaaaggggg gactggaagg gctaattcac tcccaacgaa gacaagatat ccttgatctg 2880
tggtactacc acacacaagg ctacttcctt gattggcaga actacacacc agggccaggg 2940
gtcagatata cactgacctt tggatgggtg tacaagctag taccagttga gccagataag 3000
gtagaagagg ccaataaagg agagaacacc agcttggcac accctgtgag cctgcatgga 3060
atggatgacc ctgagagaga agtggttagag tggaggtttg acagccgcct agcatttcat 3120
cacgtggccc gagagctgca tccggagtac ttcaagaact gcactagtga gccagtagat 3180
cctagactag agccctggaa gcatccagga agtcagccta aaactgcttg taccaattgc 3240
tattgtaaaa agtggtgctt tcattgccaa gtttgtttca taacagctgc cttaggcatc 3300
tcctatggca ggaagaagcg gagacagcga cgaagacctc ctcaaggcag tcagactcat 3360
caagtttctc tatcaaagca acccacctcc caatccaaag gggagccgac aggcccgaag 3420
gaataa 3426

```

<210> 83

<211> 1141

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c p17/24 mL2-Nef Tatm fusion

<400> 83

```

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
 1      5      10      15
Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
      20      25      30
Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr
      35      40      45
Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe
      50      55      60
Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile
      65      70      75      80
Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu
      85      90      95
Cys Val Thr Leu Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr
      100      105      110
Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys
      115      120      125
Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys
      130      135      140
Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp
      145      150      155      160
Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His
      165      170      175
Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu
      180      185      190
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys
      195      200      205
Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser
      210      215      220
Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu
      225      230      235      240
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp
      245      250      255
Asn Phe Met Asp Asn Thr Lys Thr Ile Val Gln Leu Asn Glu Ser
      260      265      270
Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile
      275      280      285
His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly
      290      295      300
Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn
      305      310      315      320
Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys

```

## 330

Page 52

seqlist.txt

865	Ala	Ser	Arg	Asp	Leu	870	Glu	Lys	His	Gly	Ala	875	Ile	Thr	Ser	Ser	Asn	880	Thr
					885		Ala	Cys	Ala	Trp	890	Leu	Glu	Ala	Gln	Glu	895	Glu	Glu
Ala	Ala	Thr	Asn	900	Ala	Val	Thr	Pro	905	Gln	Val	Pro	Leu	Arg	Pro	Met	910	Thr	
Glu	Val	Gly	Phe	915	Pro	Val	Thr	Pro	920	Gln	Val	Pro	Leu	Arg	Pro	Met	925	Thr	
Tyr	Lys	Ala	Ala	930	Val	Asp	Leu	Ser	935	His	Phe	Leu	Lys	Glu	Lys	Gly	940	Gly	
Leu	Glu	Gly	Leu	945	Ile	His	Ser	Gln	950	Arg	Arg	Gln	Asp	Ile	Leu	Asp	955	Leu	
Trp	Ile	Tyr	His	965	Gln	Gly	Tyr	Phe	970	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	975	Thr	
Pro	Gly	Pro	Gly	980	Val	Arg	Tyr	Pro	985	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	990	Lys	
Leu	Val	Pro	Val	995	Glu	Pro	Asp	Lys	1000	Val	Glu	Glu	Ala	Asn	Lys	Gly	1005	Glu	
Asn	Thr	Ser	Leu	1010	Ala	His	Pro	Val	1015	Ser	Leu	His	Gly	Met	Asp	Asp	1020	Pro	
Glu	Arg	Glu	Val	1025	Leu	Glu	Trp	Arg	1030	Phe	Asp	Ser	Arg	Leu	Ala	Phe	1035	His	
His	Val	Ala	Arg	1045	Glu	His	Pro	Glu	1050	Tyr	Phe	Lys	Asn	Cys	Thr	Ser	1055	Ser	
Glu	Pro	Val	Asp	1060	Pro	Arg	Leu	Glu	1065	Pro	Trp	Lys	His	Pro	Gly	Ser	1070	Gln	
Pro	Lys	Thr	Ala	1075	Cys	Thr	Asn	Cys	1080	Tyr	Cys	Lys	Lys	Cys	Cys	Phe	1085	His	
Cys	Gln	Val	Cys	1090	Phe	Ile	Thr	Ala	1095	Ala	Leu	Gly	Ile	Ser	Tyr	Gly	1100	Arg	
Lys	Lys	Arg	Arg	1105	Gln	Arg	Arg	Arg	1110	Pro	Pro	Gln	Gly	Ser	Gln	Thr	1115	His	
Gln	Val	Ser	Leu	1125	Ser	Lys	Gln	Pro	1130	Thr	Ser	Gln	Ser	Lys	Gly	Glu	1135	Pro	
Thr	Gly	Pro	Lys	1140	Glu														

<210> 84  
 <211> 4662  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 ds-gp120c RT trNef p17/24 fusion

<400> 84

atggccgagc	agctgtgggt	caccgtctac	tacggcgtgc	ctgtgtggaa	ggaggccacg	60
accaccctct	tctgcgcgag	cgacgccaa	gcctacgaca	cggaagtgc	taacgtgtgg	120
gcgacgcatg	cttgctgtgc	tacggacccc	aacccccagg	aggtgtgtgt	gggaaacgtg	180
accgagtact	tcaacatgtg	gaagaataac	atggtggatc	agatgcacga	ggacatcatc	240
tctctgtggg	accagtcctt	gaagccctgc	gtgaagctga	cgctctctct	cgtagactctg	300
gactgtgacg	acgtcaacac	caccaacagc	actaccacca	ccagcaacgg	ctggaccgga	360
gagattcgga	agggcgagat	caagaactgc	tccttcaata	tcacgacctc	gatcagagac	420
aaggtgcaga	aggaatacgc	gctgttttat	aatctcgtat	tggtccccat	cgacgacgac	480
aatgccacca	ccaagaacaa	gacgacgctg	aatttcagac	tcattcactg	caacagcagc	540
gtcatgacgc	aggcctgccc	caaggtgtcc	ttcgaaccaa	tcccgatcca	ttactgtgcc	600
cctgcccgat	tcgcgatcct	caagtgtaac	aacaagacct	tcgacgggaa	gggacctgtc	660
accaacgtca	gcacggtgca	gtgcacccat	ggcatccgcc	ccgtcgtgag	caccagctg	720
ctgctgaacg	gggtccctggc	tgaggaggag	gtggtgatcc	ggtcggacaa	cttcatggac	780
aacaccaaga	caatcatcgt	ccagctgaac	gagtcgttgg	cgattaactg	taccggcct	840
aacaacaaca	cccgtaaagg	catccacatc	gggcctggac	gggccttcta	tgccgcccgc	900
aagatcatcg	gcgacatccg	gcaggcccat	tgcaacctct	cccgcgcca	gtggaataac	960
accctgaagc	agatcgtgat	caagctgaga	gagcactttg	gaaacaagac	catcaagttc	1020
aatcagagtt	ctggcggaga	ccccgagatc	gtgcggcact	ccttcaactg	cgggggcgag	1080
ttcttctact	cgcatatcg	acagctcttc	aactccacct	ggaacggcac	cgagggcaac	1140
aacacagagg	gaaactccac	tatcaccttc	ccttgccgca	tcaagcagat	catcaacatg	1200
tggcaggagg	tgggaaaggc	catgtatgcc	ccccccatcg	ggggccagat	ccgctgctcc	1260
tccaacatca	ccggcctgct	gctcaccaga	gacgggggca	ccgagggcaa	cggcacggag	1320

seqlist.txt

```

aacgagacgg agatcttcag gcccggcggc ggcgacatga gggataactg gcggagcgag 1380
ctgtacaagt acaaggtggt gaaggtggag ccgctcggcg tggcccccac ccgggccaag 1440
cgccgcgtcg tgcagagaaat gggcccatc agtcccatcg agaccgtgcc ggtgaagctg 1500
aaaccctgga ttgacggccc caaggtcaag cagtggccac tcaccgagga gaagatcaag 1560
gccctggtgg agatctgcac cgagatggag aaagagggca agatcagcaa gatcgggcct 1620
gagaacccat acaacacccc cgtgtttgcc atcaagaaga aggacagcac caagtggcgc 1680
aagctggtgg atttccggga gctgaataag cggaccaggg atttctggga ggtccagctg 1740
ggcatccccc atccggccgg cctgaagaag aagaagagcg tgaccgtgct ggacgtgggc 1800
gacgcttact tcagcgtccc tctggacgag gactttagaa agtacaccgc ctttaccatc 1860
ccatctatca acaacgagac ccctggcatc agatatcagt acaacgtcct cccccagggc 1920
tggaagggct ctcccgccat tttccagagc tccatgacca agatcctgga gccgtttcgg 1980
aagcagaacc ccgatatcgt catctaccag tacatggacg acctgtacgt gggctctgac 2040
ctggaaatcg ggcagcatcg cacgaagatt gaggagctga ggcagcatct gctgagatgg 2100
ggcctgacca ctccgggaca gaagcatcag aaggagccgc cattcctgaa gatgggctac 2160
gagctccatc ccgacaagtg gaccgtgcag cctatcgtcc tccccgagaa ggacagctgg 2220
accgtgaacg acatccagaa gctggtgggc aagctcaact gggctagcca gatctatccc 2280
gggataaagg tgcgccagct ctgcaagctg ctgctgggca ccaaggccct gaccgaggtg 2340
atttccctca cggaggaagc cgagctcgag ctggctgaga accgggagat cctgaaggag 2400
cccgtgcacg gcgtgtacta tgacccctcc aaggacctga tcgccgaaat ccagaagcag 2460
ggccaggggc agtggacata ccagatttac caggagcctt tcaagaacct caagaccggc 2520
aagtagcccc gcatgagggg cgcccacacc aacgatgtca agcagctgac cgaggccgtc 2580
cagaagatca gaccgagtc catcgtgatc tgggggaaga caccgaagt caagctgcct 2640
atccagaagg agactggga gacgtggtgg accgaatat ggcaaggccac ctgattcccc 2700
gagtgggagt tcgtgaatac acctcctctg gtgaagctgt ggtaccagct cgagaaggag 2760
cccctcgtgg gcgcggagac attctacgtg gacggcgcgg ccaaccgcga aacaaagctc 2820
gggaaggccg ggtacgtcac caaccggggc cgccagaagg tcgtcaccct gaccgacacc 2880
accaaccaga agacggagct gcaggccatc tatctcgtc tccaggactc cggcctggag 2940
gtgaacatcg tgacggacag ccagtagcgc ctgggcatc ttcaaggcca gccggaccag 3000
tccgagagcg aactggtgaa ccagattatc gagcagctga tcaagaaaga gaaggtctac 3060
ctcgcctggg tcccggccca taagggcatt ggcggaacg agcaggtcga caagctggtg 3120
agtgcgggga ttagaaagg gctgatgggt ggttttccag tcacacctca ggtaccttta 3180
agaccaatga agctgaagg agctgtagat agctgccact ttttaaaaga aaagggggga 3240
ctggaagggc taattcactc ccaaagaaga caagatatcc ttgatctgtg gatctaccac 3300
acacaaggct acttccctga ttggcagaac tacacaccag ggccaggggt cagatatcca 3360
ctgacctttg gatggtgcta caagctagta ccagttgagc cagataaggt agaagaggcc 3420
aataaaggag agaaccaccg cttgttacac cctgtgagcc tgcatgggat ggatgacctg 3480
gagagagaag tgttagatg gaggtttgac agccgcctag catttcatca cgtggcccga 3540
gagctgcatc cggagtactt caagaactgc atgggtgccc gagcttcggt actgtctggt 3600
ggagagctgg acagatggga gaaaattagg ctgccccggg gaggcaaaaa gaaatacaag 3660
ctcaagcata tcgtgtgggc ctgaggggag ctggaacggt ttgccgtgaa cccaggcctg 3720
ctggaacatc ctgagggatg tcgccagatc ctggggcaat tgcagccatc cctccagacc 3780
gggagtgaag agctgaggtc cttgtataac acagtggcta ccctctactg cgtaaccag 3840
aggatcgaga ttaaggatac caaggaggcc ttggacaaaa ttgaggagga gcaaaacaag 3900
agcaagaaga agggccagca ggcagctgct gacactgggc atagcaacca ggtatcacag 3960
aactatccta ttgtccaaaa cattcagggc cagatgggtt atcaggccat cagccccgg 4020
acgctcaatg cctgggtgaa ggttgtcgaa gagaaggcct tttctcctga ggttatcccc 4080
atgttctccg ctttgagtga gggggccact cctcaggacc tcaatacaat gcttaatacc 4140
gtgggcggcc atcaggccgc catgcaaatg ttgaaggaga ctatcaacga ggaggcagcc 4200
gagtgggaca gagtgcattc cgtccacgct ggcccaatcg cgcccggaca gatgcgggag 4260
cctcgcggct ctgacattgc cggcaccacc tctacactgc aagagcaaat cggatggatg 4320
accaacaatc ctcccattcc agttggagaa ggtggatcat cctgggcctg 4380
aacaagatcg tgcgcatgta ctctccgaca tccatccttg acattagaca gggacccaaa 4440
gagcctttta gggattacgt cgaccggttt tataagacc tgcgagcaga gcaggcctct 4500
caggaggtca aaaactggat gacggagaca ctcctggtac agaacgctaa ccccgactgc 4560
aaaacaatct tgaaggcact aggcccggtt gccaccctgg aagagatgat gaccgcctgt 4620
caggagtag gcggaccggg acacaaaggc agagtgtgt aa 4662

```

<210> 85

<211> 1553

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 ds-gp120c RT trNef p17/24 fusion

<400> 85

Met Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp

1

5

10

15

## seqlist.txt

Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr  
 Asp Thr Glu 20 Val His Asn Val Trp 25 Ala Thr His Ala Cys 30 Val Pro Thr  
 Asp Pro Asn 35 Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe  
 Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile  
 65 Ser Leu Trp Asp Gln 70 Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu  
 Cys Val Thr Leu 85 Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr  
 Thr Thr Ser 100 Asn Gly Trp Thr Gly 105 Glu Ile Arg Lys Gly 110 Glu Ile Lys  
 Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys  
 130 Glu Tyr Ala Leu Phe Tyr 135 Asn Leu Asp Val Val Pro Ile Asp Asp Asp  
 145 Asn Ala Thr Thr Lys 150 Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His  
 Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu  
 Pro Ile Pro 180 His Tyr Cys Ala 185 Pro Ala Gly Phe Ala 190 Ile Leu Lys  
 Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser  
 Thr Val Gln Cys Thr His 215 Gly Ile Arg Pro Val Val Ser Thr Gln Leu  
 225 Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp  
 Asn Phe Met Asp Asn Thr Lys Thr Ile 250 Val Gln Leu Asn Glu Ser  
 Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile  
 His Ile Gly Pro Gly Arg Ala 295 Phe Tyr Ala Ala Arg 300 Lys Ile Ile Gly  
 Asp Ile Arg Gln Ala His 310 Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn  
 305 Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys  
 Thr Ile Lys Phe Asn Gln Ser Ser Gly 345 Gly Asp Pro Glu Ile Val Arg  
 His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln  
 Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Thr Glu Gly  
 Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met  
 385 Trp Gln Glu Val Gly 390 Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln  
 Ile Arg Cys Ser Asn Ile Thr Gly 425 Leu Leu Thr Arg Asp Gly  
 Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro  
 Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu 460 Leu Tyr Lys Tyr  
 Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys  
 465 Arg Arg Val Val Gln Arg Met Gly Pro Ile Ser Pro Ile Glu Thr Val  
 Pro Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp  
 Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu  
 Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr  
 530 Asn Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg  
 545 550 555 560

## seqlist.txt

Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp  
 565 570 575  
 Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys  
 580 585 590  
 Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu  
 595 600 605  
 Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn  
 610 615 620  
 Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly  
 625 630 635 640  
 Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu  
 645 650 655  
 Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met  
 660 665 670  
 Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr  
 675 680 685  
 Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr  
 690 695 700  
 Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Lys Met Gly Tyr  
 705 710 715 720  
 Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu  
 725 730 735  
 Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu  
 740 745 750  
 Asn Trp Ala Ser Gln Ile Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys  
 755 760 765  
 Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile Pro Leu Thr  
 770 775 780  
 Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu  
 785 790 795 800  
 Pro Val His Gly Val Tyr Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu  
 805 810 815  
 Ile Gln Lys Gln Gly Gln Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu  
 820 825 830  
 Pro Phe Lys Asn Leu Lys Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala  
 835 840 845  
 His Thr Asn Asp Val Lys Gln Leu Thr Glu Ala Val Gln Lys Ile Thr  
 850 855 860  
 Thr Glu Ser Ile Val Ile Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro  
 865 870 875 880  
 Ile Gln Lys Glu Thr Trp Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala  
 885 890 895  
 Thr Trp Ile Pro Glu Trp Glu Phe Val Asn Thr Pro Pro Leu Val Lys  
 900 905 910  
 Leu Trp Tyr Gln Leu Glu Lys Glu Pro Ile Val Gly Ala Glu Thr Phe  
 915 920 925  
 Tyr Val Asp Gly Ala Ala Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly  
 930 935 940  
 Tyr Val Thr Asn Arg Gly Arg Gln Lys Val Val Thr Leu Thr Asp Thr  
 945 950 955 960  
 Thr Asn Gln Lys Thr Glu Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp  
 965 970 975  
 Ser Gly Leu Glu Val Asn Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly  
 980 985 990  
 Ile Ile Gln Ala Gln Pro Asp Gln Ser Glu Ser Glu Leu Val Asn Gln  
 995 1000 1005  
 Ile Ile Glu Gln Leu Ile Lys Lys Glu Lys Val Tyr Leu Ala Trp Val  
 1010 1015 1020  
 Pro Ala His Lys Gly Ile Gly Gly Asn Glu Gln Val Asp Lys Leu Val  
 1025 1030 1035 1040  
 Ser Ala Gly Ile Arg Lys Val Leu Met Val Gly Phe Pro Val Thr Pro  
 1045 1050 1055  
 Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val Asp Leu Ser  
 1060 1065 1070  
 His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile His Ser Gln  
 1075 1080 1085  
 Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr Gln Gly Tyr  
 1090 1095 1100



seqlist.txt

```

Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val Arg Tyr Pro
1105      1110      1115      1120
Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu Pro Asp Lys
      1125      1130      1135
Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu His Pro Val
      1140      1145      1150
Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu Val Leu Glu Trp Arg
      1155      1160      1165
Phe Asp Ser Arg Leu Ala Phe His His Val Ala Arg Glu Leu His Pro
      1170      1175      1180
Glu Tyr Phe Lys Asn Cys Met Gly Ala Arg Ala Ser Val Leu Ser Gly
1185      1190      1195      1200
Gly Glu Leu Asp Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys
      1205      1210      1215
Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu
      1220      1225      1230
Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg
      1235      1240      1245
Gln Ile Leu Gly Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu
      1250      1255      1260
Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln
1265      1270      1275      1280
Arg Ile Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu
      1285      1290      1295
Glu Gln Asn Lys Ser Lys Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr
      1300      1305      1310
Gly His Ser Asn Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile
      1315      1320      1325
Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala
      1330      1335      1340
Trp Val Lys Val Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro
1345      1350      1355      1360
Met Phe Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr
      1365      1370      1375
Met Leu Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys
      1380      1385      1390
Glu Thr Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val
      1395      1400      1405
His Ala Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser
      1410      1415      1420
Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met
1425      1430      1435      1440
Thr Asn Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile
      1445      1450      1455
Ile Leu Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile
      1460      1465      1470
Leu Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp
      1475      1480      1485
Arg Phe Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys
      1490      1495      1500
Asn Trp Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys
1505      1510      1515      1520
Lys Thr Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met
      1525      1530      1535
Met Thr Ala Cys Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val
      1540      1545      1550
Leu

```

<210> 86  
 <211> 4662  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 RT trNef p17/24 ds gp120c fusion

## seqlist.txt

&lt;400&gt; 86

```

atggggcccca tcagtcccat cgagaccgtg ccggtgaagc tgaaaccccg gatggacggc 60
cccaagggtca agcagtggcc actcaccgag gagaagatca aggccctggt ggagatctgc 120
accgagatgg agaaagaggg caagatcagc aagatcgggc cggagaaccc atacaacacc 180
cccgtgtttg ccatcaagaa gaaggacagc accaagtggc gcaagctggt ggatttccgg 240
gagctgaata agcggaccca ggatttctgg gaggtccagc tgggcatccc ccatccggcc 300
ggcctgaaga agaagaagag cgtgaccgtg ctggacgtgg gcgacgctta cttcagcgtc 360
cctctggacg aggactttag aaagtacacc gcctttacca tcccatctat caacaacgag 420
acccctggca tcagatatca gtacaacgtc ctccccagg gctggaagg gctctccgcc 480
atthttccaga gctccatgac caagatcctg gagccgtttc ggaagcagaa ccccgatatc 540
gtcatctacc agtacatgga cgacctgtac gtgggctctg acctggaaat cgggcagcat 600
cgcacgaaga ttgaggagct gaggcagcat ctgctgagat ggggcctgac cactccggac 660
aagaagcatc agaaggagcc gccattcctg aagatgggct acgagctcca tcccgacaag 720
tggaccgtgc agcctatcgt cctccccgag aaggacagct ggaccgtgaa cgacatccag 780
aagctggtgg gcaagctcaa ctgggctagc cagatctatc ccgggatcaa ggtgcgccag 840
ctctgcaagc tgctgcgcgg caccaaggcc ctgaccgagg tgattcccct cacggaggaa 900
gccgagctcg agctggctga gaaccgggag atcttgaagg agcccgtgca cggcgtgtac 960
tattgacccct ccaaggacct gatcgccgaa atccagaagc agggccagg gcaagtggaca 1020
taccagattt accaggagcc tttcaagaac ctcaagaccg gcaagtacgc ccgcatgagg 1080
ggcggccaca ccaacgatgt caagcagctg accgaggccg tccagaagat cacgaccgag 1140
tccatcgtga tctgggggaa gacaccaag ttcaagctgc ctatccagaa ggagacctgg 1200
gagacgtggt ggaccgaata ttggcaggcc acctggattc ccgagtggga gttcgtgaat 1260
acaccttctc tgggtaagct gtggtaaccg ctcgagaagg agcccatcgt gggcgcgagg 1320
acattctacg tggacggcgc ggccaaccgc gaaacaaagc tcgggaaggc cgggtacgtc 1380
accaaccggg gccgccagaa ggtcgtcacc ctgaccgaca ccaccaacca gaagacggag 1440
ctgcaggcca tctatctcgc tctccaggac tccggcctgg aggtgaacat cgtgacggac 1500
agccagtacg cgctgggcat tattcaggcc cagccggacc agtccgagag cgaactggtg 1560
aaccagatta tcgagcagct gatcaagaaa gagaaggctt acctcgctg ggtcccggcc 1620
cataagggca ttggcgga caagcaggtc gacaagctgg tgagtgcggg gattagaaag 1680
gtgctgatgg tgggttttcc agtcacacct caggtacctt taagaccaat gacttacaag 1740
gcagctgtag atcttagcca ctttttaaaa gaaaaggggg gactggaagg gctaattcac 1800
tcccaagaa gacaagatat ccttgatctg tggatctacc acacacaagg ctacttccct 1860
gattggcaga actacacacc agggccaggg gtcagatatc cactgacctt tggatggtgc 1920
tacaagctag taccagttag gccagataag gtagaagagg ccaataaagg agagaacacc 1980
agcttggttac accctgtgag cctgcatggg atggatgacc cggagagaga agtgtagag 2040
tggaggtttg acagccgcct agcatttcac cactgtggcc gagagctgca tccggagtag 2100
ttcaagaact ccagcgttgc ccagccttcg gactgtctct gtggagagct ggacagatgg 2160
gagaaaatta ggctgcgccc gggaggcaaa agaaatata agctcaagca tatcgtgtgg 2220
gcctcgaggg agcttgaacg gtttgccgtg aacccaggcc tgctggaaac atctgaggga 2280
tgctcgccaga tcctggggca attgcagcca tccctccaga ccgggagtga agagctgagg 2340
tccttgtaga acacttgagg tacctctac tgcgtacacc agaggatcga gattaaggat 2400
accaaggagg ccttggaaca aattgaggag gagcaaaaca agagcaagaa gaaggcccag 2460
caggcagctg ctgacactgg gcatagcaac caggtatcac agaactatcc tattgtccaa 2520
aacattcagg gccagatggg tcatcaggcc atcagcccc ggacgctcaa tgcctgggtg 2580
aaggttgctg aagagaaggc cttttctctc gaggttatcc ccatgttctc cgctttgagt 2640
gagggggcca ctctcagga cctcaataca atgtttaata ccgtggggcg ccatcaggcc 2700
gccatgcaaa tgttgaagga gactatcaac gaggaggcag ccgagtggga cagagtgcac 2760
cccgtccacg ctggcccaat cgcgcccgga cagatgcggg agcctcgcgg ctctgacatt 2820
gccggcacca cctctacact gcaagagcaa atcggatgga tgaccaacaa tcttcccatc 2880
ccagttggag aaatctataa acggtggatc atcttgggcc tgaacaagat cgtgcgcag 2940
tactctccga catccatcct tgacattaga cagggacca aagagccttt tagggattac 3000
gtcgaccggt tttataagac cctgcgagca gagcaggcct ctcaggagg tcaaaaactgg 3060
atgacggaga cactcctggt acagaacgct aaccccgact gcaaaaacaat cttgaaggca 3120
ctaggcccgg ctgccacctt ggaagagatg atgaccgctt gtcagggagt aggcggacc 3180
ggacacaaag ccagagtgtt gatggccgag cagctgtggg tcaccgtcta ctacggcgtg 3240
cctgtgtgga aggaggccac gaccacctc ttctgcgcga gcgacgcaa ggcctacgac 3300
acggaagtgc ataactgtgt ggcgacgat gcttgctgtc ctacggaccc caacccccag 3360
gaggtggtgc tgggaaacgt gaccgagtac ttcaacatgt ggaagaataa catggtggat 3420
cagatgcacg aggacatcat ctctctgtgg gaccagtccc tgaagccctg cgtgaagctg 3480
acgcctctct gcgtgtgact gagctcaaca cagctcaaca ccaccaacag cactaccacc 3540
accagcaacg gctggaccgg agagattcgg aagggcgaga tcaagaactg ctcttcaat 3600
atcacgacct cgatcagaga caaggtgcag aaggaatacg cgctgtttta taatctcgat 3660
gtggtcccca tcgacgacga caatgccacc accaagaaca agacgacgcg taatttcaga 3720
ctctactact gcaacagcag cgtcatgagc caggctgcc ccaaggtgtc cttcgaacca 3780
atcccgatcc attactgtgc cctgcggga ttcgcgatcc tcaagtgtaa caacaagacc 3840
ttcgacggga agggcctgtg caccaacgtc agcacggtgc agtgaccca tggcatccgc 3900
cccgtcgtga gcacccagct gctgctgaac gggctcctgg ctgaggagga ggtggtgatc 3960
cggtcggaca acttcatgga caacaccaag acaatcatcg tccagctgaa cgagtctgtg 4020

```

seqlist.txt

```

gcgattaact gtacccggcc taacaacaac acccgtaagg gcatccacat cgggcctgga 4080
cgggccttct atgccgcccg caagatcatc ggcgacatcc ggcaggccca ttgcaacctc 4140
tcccgcgccc agtggaataa caccctgaag cagatcgtga tcaagctgag agagcacttt 4200
ggaaacaaga ccatcaagtt caatcagagt tctggcggag accccgagat cgtgcggcac 4260
tccttcaact gcgggggcgga gttcttctac tgcgatacga cacagctctt caactccacc 4320
tggaacggca ccgaggggcaa caacacagag ggaaactcca ctatcacctt cccttgccgc 4380
atcaagcaga tcatcaacat gtggcaggag gtgggaaagg ccatgtatgc ccccccatc 4440
ggggggccaga tccgctgctc ctccaacatc accggcctgc tgctcaccag agacgggggc 4500
accgagggca acggcacgga gaacgagacg gagatcttca ggcccggcgg cggcgacatg 4560
agggataact ggcggagcga gctgtacaag tacaaggtgg tgaagggtga gccgctcggc 4620
gtggcccccga cccggggccaa gcgccgcgctc gtgcagagat ga 4662

```

<210> 87

<211> 1553

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 RT trNef p17/24 ds gp120c fusion

<400> 87

```

Met Gly Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro
1      5      10      15
Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys
20     25     30
Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Gly Lys
35     40     45
Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala
50     55     60
Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg
65     70     75     80
Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
85     90     95
Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp
100    105    110
Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys
115    120    125
Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile
130    135    140
Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala
145    150    155    160
Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln
165    170    175
Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly
180    185    190
Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg
195    200    205
Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln
210    215    220
Lys Glu Pro Pro Phe Leu Lys Met Gly Tyr Glu Leu His Pro Asp Lys
225    230    235    240
Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val
245    250    255
Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
260    265    270
Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr
275    280    285
Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu
290    295    300
Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
305    310    315    320
Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
325    330    335
Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
340    345    350
Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
355    360    365
Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile

```

## seqlist.txt

	370					375				380					
Trp	Gly	Lys	Thr	Pro	Lys	Phe	Lys	Leu	Pro	Ile	Gln	Lys	Glu	Thr	Trp
385					390					395					400
Glu	Thr	Trp	Trp	Thr	Glu	Tyr	Trp	Gln	Ala	Thr	Trp	Ile	Pro	Glu	Trp
				405					410					415	
Glu	Phe	Val	Asn	Thr	Pro	Pro	Leu	Val	Lys	Leu	Trp	Tyr	Gln	Leu	Glu
			420					425					430		
Lys	Glu	Pro	Ile	Val	Gly	Ala	Glu	Thr	Phe	Tyr	Val	Asp	Gly	Ala	Ala
		435					440					445			
Asn	Arg	Glu	Thr	Lys	Leu	Gly	Lys	Ala	Gly	Tyr	Val	Thr	Asn	Arg	Gly
	450					455					460				
Arg	Gln	Lys	Val	Val	Thr	Leu	Thr	Asp	Thr	Thr	Asn	Gln	Lys	Thr	Glu
465					470					475					480
Leu	Gln	Ala	Ile	Tyr	Leu	Ala	Leu	Gln	Asp	Ser	Gly	Leu	Glu	Val	Asn
			485						490					495	
Ile	Val	Thr	Asp	Ser	Gln	Tyr	Ala	Leu	Gly	Ile	Ile	Gln	Ala	Gln	Pro
			500					505					510		
Asp	Gln	Ser	Glu	Ser	Glu	Leu	Val	Asn	Gln	Ile	Ile	Glu	Gln	Leu	Ile
		515					520					525			
Lys	Lys	Glu	Lys	Val	Tyr	Leu	Ala	Trp	Val	Pro	Ala	His	Lys	Gly	Ile
	530					535					540				
Gly	Gly	Asn	Glu	Gln	Val	Asp	Lys	Leu	Val	Ser	Ala	Gly	Ile	Arg	Lys
545					550					555					560
Val	Leu	Met	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro
			565						570					575	
Met	Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys
			580					585					590		
Gly	Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu
		595				600						605			
Asp	Leu	Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn
	610					615					620				
Tyr	Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys
625					630					635					640
Tyr	Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys
			645						650					655	
Gly	Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp
			660					665					670		
Asp	Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala
		675					680					685			
Phe	His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys
	690					695					700				
Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly	Gly	Glu	Leu	Asp	Arg	Trp
705					710					715					720
Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Lys	Tyr	Lys	Leu	Lys
			725						730					735	
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Arg	Phe	Ala	Val	Asn	Pro	
			740					745				750			
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu
		755					760					765			
Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn
	770					775					780				
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile	Lys	Asp
785					790					795					800
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Gln	Asn	Lys	Ser	Lys	
			805						810					815	
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn	Gln	Val
			820					825					830		
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His
		835					840					845			
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
	850					855					860				
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser
865					870					875					880
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly
			885						890					895	
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu
			900					905					910		
Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala

## seqlist.txt

```

915          920          925
Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
930          935          940
Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
945          950          955
Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
965          970          975
Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
980          985          990
Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
995          1000          1005
Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
1010          1015          1020
Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
1025          1030          1035
Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
1045          1050          1055
Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Met Ala Glu Gln Leu
1060          1065          1070
Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr Thr
1075          1080          1085
Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val His
1090          1095          1100
Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln
1105          1110          1115
Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe Asn Met Trp Lys Asn
1125          1130          1135
Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln
1140          1145          1150
Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu Asp
1155          1160          1165
Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr Thr Ser Asn Gly
1170          1175          1180
Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe Asn
1185          1190          1195
Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu Phe
1205          1210          1215
Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp Asn Ala Thr Thr Lys
1220          1225          1230
Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His Cys Asn Ser Ser Val
1235          1240          1245
Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His
1250          1255          1260
Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr
1265          1270          1275
Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser Thr Val Gln Cys Thr
1285          1290          1295
His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser
1300          1305          1310
Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp Asn Phe Met Asp Asn
1315          1320          1325
Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Ala Ile Asn Cys
1330          1335          1340
Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro Gly
1345          1350          1355
Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly Asp Ile Arg Gln Ala
1365          1370          1375
His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn Thr Leu Lys Gln Ile
1380          1385          1390
Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys Thr Ile Lys Phe Asn
1395          1400          1405
Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg His Ser Phe Asn Cys
1410          1415          1420
Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln Leu Phe Asn Ser Thr
1425          1430          1435
Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly Asn Ser Thr Ile Thr
1445          1450          1455
Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val Gly

```

seqlist.txt

```

      1460      1465      1470
Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln Ile Arg Cys Ser Ser
      1475      1480      1485
Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Thr Glu Gly Asn
      1490      1495      1500
Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp Met
1505      1510      1515      1520
Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Val
      1525      1530      1535
Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Val Val Gln
      1540      1545      1550
Arg

```

```

<210> 88
<211> 2424
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> HIV-1 gp120c Nef Tatm fusion

```

```

<400> 88
atgaaggtca aggagaccag aaagaactac cagcatctgt ggcgctgggg caccatgctc 60
ctgggaatgc tgatgatctg ctccgccgcc gagcagctgt gggtcaccgt ctactacggc 120
gtgcctgtgt ggaaggaggc cacgaccacc ctcttctgcg cgagcgacgc caaggcctac 180
gacacggaag tgcataacgt gtgggcgacg catgcttgcg tgcctacgga cccaacccc 240
caggaggtgg tgcctggaaa cgtgaccgag tacttcaaca tctggaagaa taacatggtg 300
gatcagatgc acgaggacat catctctctg tgggaccagt ccctgaagcc ctgctgtaag 360
ctgacgcctc tctgctgac actggactgt gacgacgtca acaccaccaa cagcactacc 420
accaccagca acggtggac cggagagatt cggaaggcg agatcaagaa ctgctccttc 480
aatatcacga cctcgatcag agacaagggt cagaaggaa acgcgctgtt ttataatctc 540
gatgtggtcc ccacgcacga cgacaatgcc accaccaaga acaagacgac gcgtaatttc 600
agatcattc actgcaacag cagcgtcatg acgcaggcct gccccaaagg gtctctcgaa 660
ccaatccga tccattactg tgcccctgcc ggattcgcga tcctcaagt taacaacaag 720
accttcgacg ggaaggccct gtgcaccaac gtcagcacgg tgcagtgcac ccatggcatc 780
cgccccgtcg tgagcaccca gctgctgctg aacgggtccc tggctgagga ggaggtggtg 840
atccggtcgg acaacttcat ggacaacacc aagacaatca tcgtccagct gaacgagtct 900
gtggcgatta actgtaccgg gcctaacaac aacaccgcta agggcatcca catcgggcct 960
ggacgggcct tctatgccgc ccgcaagatc atcggcgaca tccggcaggc ccattgcaac 1020
ctctcccgcg cccagtggaa taacaccctg aagcagatcg tgatcaagct gagagagcac 1080
tttgaaaca agaccatcaa gttcaatcag agttctggcg gagaccccga gatcgtgcgg 1140
cactccttca actgcggggg cgagttcttc tactgcgata cgacacagct cttcaactcc 1200
acctggaacg gcaccgaggg caacaacaca gagggaaact ccactatcac cctcccttgc 1260
cgcatcaagc agatcatcaa catgtggcag gaggtgggaa aggccatgta tgccccccc 1320
atcgggggcc agatccgctg ctcttccaac atcaccggcc tgctgctcac cagagacggg 1380
ggcaccgagg gcaacggcac ggagaacgag acggagatct tcaggcccgg cggcggcgac 1440
atgagggata actggcggag cgagctgtac aagtacaagg tgggtgaagg ggagccgctc 1500
ggcgtggccc ccacccgggc caagcgccgc gtcgtgcaga gaatgggtgg caagtggta 1560
aaaagtagtg tggttggatg gcctactgta agggaaagaa tgagacgagc tgagccagca 1620
gcagatgggg tgggagcagc atctcgagac ctggaaaaac atggagcaat cacaagtagc 1680
aatacagcag ctaccaatgc tgcttggtgcc tggctagaag cacaagagga ggaggaggtg 1740
ggttttccag tcacacctca ggtaccttta agaccaatga cttacaaggc agctgtagat 1800
cttagccact ttttaaaaga aaagggggga ctggaagggc taattcactc ccaacgaaga 1860
caagatatcc ttgatctgtg gatctaccac acacaaggct acttccctga ttggcagaac 1920
tacacaccag ggccaggggg cagatatcca ctgacctttg gatggtgcta caagctagta 1980
ccagttgagc cagataaggt agaagaggcc aataaaggag agaaccaccag cttgttacac 2040
cctgtgagcc tgcattgaaat ggatgacctt gagagagaag tgttagagtg gaggtttgac 2100
agcgcctag cgtggcccga cgtgtgcac cgagtagtct caagaactgc 2160
actagtgagc cagtagatcc tagactagag ccctggaagc atccaggaag tcagcctaaa 2220
actgcttgta ccaattgcta ttgtaaaaag tgttgcttcc attgccaagt ttgtttcata 2280
acagctgcct taggcatctc ctatggcagg aagaagcgga gacagcgacg aagacctcct 2340
caaggcagtc agactcatca agtttctcta tcaaagcaac ccacctccca atccaaaggg 2400
gagccgacag gcccgaaagga ataa 2424

```

```

<210> 89
<211> 807

```

## seqlist.txt

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; HIV-1 gp120c Nef Tatm fusion

&lt;400&gt; 89

```

Met Lys Val Lys Glu Thr Arg Lys Asn Tyr Gln His Leu Trp Arg Trp
 1      5      10      15
Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Ala Glu Gln
 20      25      30
Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
 35      40      45
Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val
 50      55      60
His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65      70      75
Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe Asn Met Trp Lys
 85      90      95
Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100      105      110
Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115      120      125
Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr Thr Thr Ser Asn
130      135      140
Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe
145      150      155
Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu
165      170      175
Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp Asn Ala Thr Thr
180      185      190
Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His Cys Asn Ser Ser
195      200      205
Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
210      215      220
His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys
225      230      235
Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser Thr Val Gln Cys
245      250      255
Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
260      265      270
Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp Asn Phe Met Asp
275      280      285
Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Ala Ile Asn
290      295      300
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro
305      310      315
Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly Asp Ile Arg Gln
325      330      335
Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn Thr Leu Lys Gln
340      345      350
Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys Thr Ile Lys Phe
355      360      365
Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg His Ser Phe Asn
370      375      380
Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln Leu Phe Asn Ser
385      390      395
Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly Asn Ser Thr Ile
405      410      415
Thr Leu Pro Cys Arg Ile Lys Gln Ile Asn Met Trp Gln Glu Val
420      425      430
Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln Ile Arg Cys Ser
435      440      445
Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Thr Glu Gly
450      455      460
Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp
465      470      475
Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys
480

```

seq11st.txt										seq12st.txt									
Val	Glu	Pro	Leu	485 Gly	Val	Ala	Pro	Thr	490 Arg	Ala	Lys	Arg	Arg	495 Val	Val				
Gln	Arg	Met	500 Gly	Gly	Lys	Trp	Ser	505 Lys	Ser	Ser	Val	Val	510 Gly	Trp	Pro				
Thr	Val	Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala	Asp	Gly	Val				
Gly	Ala	Ala	Ser	Arg	Asp	535 Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	560 Ser				
Asn	Thr	Ala	Ala	Thr	550 Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	575 Glu				
Glu	Glu	Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro				
Met	Thr	Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys				
Gly	Gly	Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu				
Asp	Leu	Trp	Ile	Tyr	His	615 Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn				
Tyr	Thr	Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	640 Cys				
Tyr	Lys	Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys				
Gly	Glu	Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp				
Asp	Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala				
Phe	His	His	Val	Ala	Arg	710 Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	720 Cys				
Thr	Ser	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	735 Gly				
Ser	Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys				
Phe	His	Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	Leu	Gly	Ile	Ser	Tyr				
Gly	Arg	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln				
Thr	His	Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Lys	Gly				
Glu	Pro	Thr	Gly	Pro	Lys	Glu				795					800				

```
<210> 90
<211> 2424
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> HIV-1 Nef Tatm gp120c fusion

<400>	90						
atgggtggca	agtgggtcaaa	aagtagtggtg	gttgatggc	ctactgtaag	ggaaagaatg	60	
agacgagctg	agccagcagc	agatgggggtg	ggagcagcat	ctcgagacct	ggaaaacat	120	
ggagcaatca	caagtagcaa	tacagcagct	accaatgctg	cttggtccctg	gctagaagca	180	
caagaggagg	aggaggtggg	ttttccagtc	accactcagg	tacctttaag	accaatgact	240	
tacaaggcag	ctgtagatct	tagccacttt	ttaaaagaaa	aggggggact	ggaagggtac	300	
attcactccc	aacgaagaca	agatatcctt	gatctgtgga	tctaccacac	acaaggctac	360	
ttccctgatt	ggcagaacta	cacaccaggg	cgagggtgtc	gatatccact	gacctttgga	420	
tgggtctaca	agctagatcc	agttgagcca	gataaggtag	aagaggccaa	taaaggagag	480	
aacaccagct	tgttacaccc	tgtgagcctg	catggaatgg	atgaccctga	gagagaagtg	540	
ttagagtggg	ggtttgacag	ccgcctagca	tttcatcacg	tggccccaga	gctgcatccg	600	
gagtacttca	agaactgcac	tagttagcca	gtagactcta	gactagagcc	ctggaagcat	660	
ccaggaagtc	agcctaaaac	tgcttgtagc	aattgctatt	gtaaaaagtg	ttgctttcat	720	
tgccaagttt	gtttcataac	agctgcctta	ggcatctcct	atggcaggaa	gaagcggaga	780	
cagcgacgaa	gacctctcta	aggcagtcag	actcatcaag	tttctctatc	aaagcaaccc	840	
acctcccaat	ccaaagggga	gccgacaggc	ccgaaggaaa	tgaaggctca	ggagaccaga	900	
aagaactacc	agcatctgtg	cgctgtgggc	accatgtctc	tgggaatgct	gatgatctgc	960	



seqlist.txt

```
tccgccgccg agcagctgtg ggtcaccgtc tactacggcg tgcctgtgtg gaaggaggcc 1020
acgaccaccc tcttctgctg gagcgacgcc aaggcctacg acacggaagt gcataacgtg 1080
tgggcgacgc atgcttgctg gcctacggac cccaaccccc aggaggtggt gctgggaaac 1140
gtgaccgagt acttcaacat gtggaagaat aacatggtgg atcagatgca cgaggacatc 1200
atctctctgt gggaccagtc cctgaagccc tgcgtgaagc tgacgcctct ctgctgaca 1260
ctggactgtg acgacgtcaa caccaccaac agcactacca ccaccagcaa cggctggacc 1320
ggagagattc ggaagggcga gatcaagaac tgctccttca atatcacgac ctcgatcaga 1380
gacaaggtgc agaaggaata cgcgctgttt tataatctcg atgtggtccc catcgacgac 1440
gacaatgcca ccaccaagaa caagacgacg cgtaatttca gactcattca ctgcaacagc 1500
agcgtcatga cgcaggcctg cccaaggtg tccttcgaac caatcccgat ccattactgt 1560
gcccctgccg gattcgcgat cctcaagtgt aacaacaaga ccttcgacgg gaagggcctg 1620
tgcaccaacg tcagcacggt gcagtgcacc catggcatcc gccccgtcgt gagcaccag 1680
ctgctgtctg acgggtccct ggctgaggag gaggtggtga tccggtcggg caacttcgat 1740
gacaacacca agacaatcat cgtccagctg aacgagctct tggcgattaa ctgtaccgag 1800
cctaacaaca acaccgtaa gggcatccac atcgggcctg gacgggcctt ctatgccgcc 1860
cgcaagatca tcggcgacat ccggcaggcc cattgcaacc tctcccgcgc ccagtgggat 1920
aacaccctga agcagatcgt gatcaagctg agagagcact ttggaacaaa gaccatcaag 1980
ttcaatcaga gttctggcgg agaccccagc atcgtgcggc actccttcaa ctgagggggc 2040
gagttcttct actcgatcgc gacacagctc ttcaactcca cctggaacgg caccgagggc 2100
aacaacacag agggaaactc cactatcacc ctcccttgcc gcatcaagca gatcatcaac 2160
atgtggcagg aggtgggaaa ggccatgtat gcccccccca tcgggggcca gatccgctgc 2220
tcctccaaca tcaccggcct gctgctcacc agagacgggg gcaccgaggg caacggcacg 2280
gagaacgaga cggagatctt caggcccggc ggcggcgaca tgagggataa ctggcgagc 2340
gagctgtaca agtacaaggt ggtgaaggtg gagccgctcg gcgtggcccc caccggggcc 2400
aagcgccgcg tcgtgcagag atga 2424
```

<210> 91

<211> 807

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 Nef Tatm gp120c fusion

<400> 91

```
Met Gly Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val
1 5 10 15
Arg Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala
20 25 30
Ala Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Asn Thr
35 40 45
Ala Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu
50 55 60
Glu Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr
65 70 75 80
Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly
85 90 95
Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu
100 105 110
Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr
115 120 125
Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys
130 135 140
Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu
145 150 155 160
Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro
165 170 175
Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His
180 185 190
His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser
195 200 205
Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln
210 215 220
Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His
225 230 235 240
Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg
245 250 255
Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His
```

## seqlist.txt

```

      260      265      270
Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro
  275      280      285
Thr Gly Pro Lys Glu Met Lys Val Lys Glu Thr Arg Lys Asn Tyr Gln
  290      295      300
His Leu Trp Arg Trp Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys
  305      310      315      320
Ser Ala Ala Glu Gln Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val
      325      330      335
Trp Lys Glu Ala Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala
      340      345      350
Tyr Asp Thr Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro
      355      360      365
Thr Asp Pro Asn Pro Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr
      370      375      380
Phe Asn Met Trp Lys Asn Asn Met Val Asp Gln Met His Glu Asp Ile
  385      390      395      400
Ile Ser Leu Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro
      405      410      415
Leu Cys Val Thr Leu Asp Cys Asp Val Asn Thr Thr Asn Ser Thr
      420      425      430
Thr Thr Thr Ser Asn Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile
      435      440      445
Lys Asn Cys Ser Phe Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln
      450      455      460
Lys Glu Tyr Ala Leu Phe Tyr Asn Leu Asp Val Pro Ile Asp Asp
  465      470      475      480
Asp Asn Ala Thr Thr Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile
      485      490      495
His Cys Asn Ser Ser Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe
      500      505      510
Glu Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu
      515      520      525
Lys Cys Asn Asn Lys Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val
      530      535      540
Ser Thr Val Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln
  545      550      555      560
Leu Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser
      565      570      575
Asp Asn Phe Met Asp Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu
      580      585      590
Ser Val Ala Ile Asn Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly
      595      600      605
Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile
      610      615      620
Gly Asp Ile Arg Gln Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn
  625      630      635      640
Asn Thr Leu Lys Gln Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn
      645      650      655
Lys Thr Ile Lys Phe Asn Gln Ser Ser Gly Glu Phe Phe Tyr Cys Asp Thr Thr
      660      665      670
Arg His Ser Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr
      675      680      685
Gln Leu Phe Asn Ser Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu
      690      695      700
Gly Asn Ser Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn
  705      710      715      720
Met Trp Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly
      725      730      735
Gln Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp
      740      745      750
Gly Gly Thr Glu Gly Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg
      755      760      765
Pro Gly Gly Gly Asp Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys
      770      775      780
Tyr Lys Val Val Lys Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala
  785      790      795      800
Lys Arg Arg Val Val Gln Arg

```

805

<210> 92  
 <211> 2232  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 trNef Tatm gp120c fusion

<400> 92  
 atggtgggtt ttccagtcac acctcaggtta cttttaagac caatgactta caaggcagct 60  
 gtagatccta gccactttttt aaaagaaaag gggggactgg aagggtctaat tcactcccaa 120  
 cgaagacaag atatccttga tctgtggatc taccacacac aaggctactt ccctgattgg 180  
 cagaactaca caccagggcc aggggtcaga tatccactga cctttggatg gtgctacaag 240  
 ctagtaccag ttgagccaga taaggtagaa gaggccaata aaggagagaa caccagcttg 300  
 ttacaccctg tgagcctgca tggaatggat gacctgaga gagaagtgtt agagtggagg 360  
 tttgacagcc gcctagcatt tcatcacgtg gcccgagagc tgcattccgga gtacttcaag 420  
 aactgcacta gtgagccagt agatcctaga ctagagccct ggaagcatcc aggaagtcat 480  
 cctaaaactg cttgtaccaaa ttgctattgt aaaaagtgtt gctttcattg ccaagtttgt 540  
 ttcataacag ctgccttagg catctcctat ggcaggaaga agcggagaca gcgacgaaga 600  
 cctcctcaag gcagtcagac tcatcaagtt tctctatcaa agcaaccac ctccaatcc 660  
 aaaggggagc cgacagggcc gaaggaaatg aagggtcaagg agaccagaaa gaactaccag 720  
 catctgtggc gctggggcac catgctcctg ggaatgctga tgatctgctc cgccgccgag 780  
 cagctgtggg tcaccgtcta ctacggcgtg cctgtgtgga aggaggccac gaccaccctc 840  
 ttctgctgca ggcagcccaa ggcctacgac acggaagtgc ataactgtgt ggcgacgat 900  
 gcttgctgca ctacggaccc caaccccag gaggtgtgct tgggaaacgt gaccgagtac 960  
 ttcaacatgt ggaagaataa catggtggat cagatgcacg aggacatcat ctctctgttg 1020  
 gaccagtccc tgaagccctg cgtgaagctg acgcctctct gcgtgacact ggactgtgac 1080  
 gacgtcaaca ccaccaacag cactaccacc accagcaacg gctggaccgg agagattcgg 1140  
 aagggcgaga tcaagaactg ctcttcaat atcacgacct cgatcagaga caaggtgcag 1200  
 aaggaatacg cgctgtttta taatctcgat gtggtcccca tcgacgacga caatgccacc 1260  
 accaagaaca agacgacgca taatttcaga ctcttcaact gcaacagcag cgtcatgacg 1320  
 caggcctgcc ccaaggtgtc cttcgaacca atcccgatcc attactgtgc ccctgcccga 1380  
 ttctgcgatcc tcaagtgtaa caacaagacc ttcgacggga agggcctgtg caccaacgct 1440  
 agcacggtgc agtgcaccca tggcatccgc cccgtcgtga gcacccagct gctgctgaac 1500  
 ggggtccctg ctgaggagga ggtggtgatc cggctcgaca acttcatgga caacaccaag 1560  
 acaatcatcg tccagctgaa cgagtctgtg gcgattaact gtacccggcc taacaacaac 1620  
 acccgtaagg gcatccacat cgggccttga cgggccttct atgccggccg caagatcatc 1680  
 ggcgacatcc ggcaggccca ttgcaacctc tccgcgccc agtggataaa caccctgaag 1740  
 cagatcgtga tcaagctgag agagcacttt ggaacaaga ccatcaagtt caatcagagt 1800  
 tctggcggag accccgagat cgtgcggcac tcttcaact gcgggggcga gttcttctac 1860  
 tgcgatacga cacagctctt caactccacc tggaaacgga ccgagggcaa caacacagag 1920  
 ggaaactcca ctatcacctc cccttgccgc atcaagcaga tcatcaacat gtggcaggag 1980  
 gtgggaaagg ccatgtatgc ccccccatc agggggcaga tccgctgctc ctccaacatc 2040  
 accggcctgc tgctcaccag agacgggggc accgagggca acggcacgga gaacgagacg 2100  
 gagatcttca ggcccggcgg cggcgacatg agggataact ggcgagcga gctgtacaag 2160  
 tacaaggtgg tgaaggtgga gccgctcggc gtggcccca cccgggcaa gcgccgcgtc 2220  
 gtgcagagat ga 2232

<210> 93  
 <211> 743  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 trNef Tatm gp120c fusion

<400> 93  
 Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr  
 1 5 10 15  
 Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly  
 20 25 30  
 Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu  
 35 40 45  
 Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr  
 50 55 60

## seq1ist.txt

Pro 65	Gly	Pro	Gly	Val	Arg 70	Tyr	Pro	Leu	Thr	Phe 75	Gly	Trp	Cys	Tyr	Lys 80
Leu	Val	Pro	Val	Glu 85	Pro	Asp	Lys	Val	Glu 90	Glu	Ala	Asn	Lys	Gly 95	Glu
Asn	Thr	Ser	Leu 100	Leu	His	Pro	Val	Ser 105	Leu	His	Gly	Met	Asp 110	Asp	Pro
Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg 120	Phe	Asp	Ser	Arg	Leu 125	Ala	Phe	His
His	Val 130	Ala	Arg	Glu	Leu	His 135	Pro	Glu	Tyr	Phe	Lys 140	Asn	Cys	Thr	Ser
Glu 145	Pro	Val	Asp	Pro	Arg 150	Leu	Glu	Pro	Trp	Lys 155	His	Pro	Gly	Ser	Gln 160
Pro	Lys	Thr	Ala	Cys 165	Thr	Asn	Cys	Tyr	Cys 170	Lys	Lys	Cys	Cys	Phe 175	His
Cys	Gln	Val	Cys 180	Phe	Ile	Thr	Ala	Ala 185	Leu	Gly	Ile	Ser	Tyr 190	Gly	Arg
Lys	Lys	Arg 195	Arg	Gln	Arg	Arg	Arg 200	Pro	Pro	Gln	Gly	Ser 205	Gln	Thr	His
Gln	Val 210	Ser	Leu	Ser	Lys	Gln 215	Pro	Thr	Ser	Gln	Ser 220	Lys	Gly	Glu	Pro
Thr 225	Gly	Pro	Lys	Glu	Met 230	Lys	Val	Lys	Glu	Thr 235	Arg	Lys	Asn	Tyr	Gln 240
His	Leu	Trp	Arg	Trp 245	Gly	Thr	Met	Leu	Leu 250	Gly	Met	Leu	Met	Ile 255	Cys
Ser	Ala	Ala	Glu 260	Gln	Leu	Trp	Val	Thr 265	Val	Tyr	Tyr	Gly	Val 270	Pro	Val
Trp	Lys	Glu 275	Ala	Thr	Thr	Thr	Leu 280	Phe	Cys	Ala	Ser	Asp 285	Ala	Lys	Ala
Tyr	Asp 290	Thr	Glu	Val	His	Asn 295	Val	Trp	Ala	Thr	His 300	Ala	Cys	Val	Pro
Thr 305	Asp	Pro	Asn	Pro	Gln 310	Glu	Val	Val	Leu	Gly 315	Asn	Val	Thr	Glu	Tyr 320
Phe	Asn	Met	Trp	Lys 325	Asn	Asn	Met	Val	Asp 330	Gln	Met	His	Glu	Asp 335	Ile
Ile	Ser	Leu	Trp 340	Asp	Gln	Ser	Leu	Lys 345	Pro	Cys	Val	Lys	Leu 350	Thr	Pro
Leu	Cys	Val 355	Thr	Leu	Asp	Cys	Asp 360	Asp	Val	Asn	Thr	Thr 365	Asn	Ser	Thr
Thr	Thr 370	Thr	Ser	Asn	Gly	Trp 375	Thr	Gly	Glu	Ile	Arg 380	Lys	Gly	Glu	Ile
Lys 385	Asn	Cys	Ser	Phe	Asn 390	Ile	Thr	Thr	Ser	Ile 395	Arg	Asp	Lys	Val	Gln 400
Lys	Glu	Tyr	Ala	Leu 405	Phe	Tyr	Asn	Leu	Asp 410	Val	Val	Pro	Ile	Asp 415	Asp
Asp	Asn	Ala	Thr 420	Thr	Lys	Asn	Lys	Thr 425	Thr	Arg	Asn	Phe	Arg 430	Leu	Ile
His	Cys	Asn 435	Ser	Ser	Val	Met	Thr 440	Gln	Ala	Cys	Pro	Lys 445	Val	Ser	Phe
Glu	Pro 450	Ile	Pro	Ile	His	Tyr 455	Cys	Ala	Pro	Ala	Gly 460	Phe	Ala	Ile	Leu
Lys 465	Cys	Asn	Asn	Lys	Thr 470	Phe	Asp	Gly	Lys	Gly 475	Leu	Cys	Thr	Asn	Val 480
Ser	Thr	Val	Gln	Cys 485	Thr	His	Gly	Ile	Arg 490	Pro	Val	Val	Ser	Thr 495	Gln
Leu	Leu	Leu	Asn 500	Gly	Ser	Leu	Ala	Glu 505	Glu	Glu	Val	Val	Ile 510	Arg	Ser
Asp	Asn	Phe 515	Met	Asp	Asn	Thr	Lys 520	Thr	Ile	Ile	Val	Gln 525	Leu	Asn	Glu
Ser	Val 530	Ala	Ile	Asn	Cys	Thr 535	Arg	Pro	Asn	Asn	Asn 540	Thr	Arg	Lys	Gly
Ile 545	His	Ile	Gly	Pro	Gly 550	Arg	Ala	Phe	Tyr	Ala 555	Ala	Arg	Lys	Ile	Ile 560
Gly	Asp	Ile	Arg	Gln 565	Ala	His	Cys	Asn	Leu 570	Ser	Arg	Ala	Gln	Trp 575	Asn
Asn	Thr	Leu	Lys 580	Gln	Ile	Val	Ile	Lys 585	Leu	Arg	Glu	His	Phe 590	Gly	Asn
Lys	Thr	Ile 595	Lys	Phe	Asn	Gln	Ser 600	Ser	Gly	Gly	Asp	Pro 605	Glu	Ile	Val

seqlist.txt

Arg	His	Ser	Phe	Asn	Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr
	610					615					620				
Gln	Leu	Phe	Asn	Ser	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu
625					630					635					640
Gly	Asn	Ser	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile	Asn
				645					650					655	
Met	Trp	Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly
			660					665					670		
Gln	Ile	Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp
		675					680					685			
Gly	Gly	Thr	Glu	Gly	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg
	690					695					700				
Pro	Gly	Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys
705					710					715					720
Tyr	Lys	Val	Val	Lys	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala
				725					730					735	
Lys	Arg	Arg	Val	Val	Gln	Arg									
			740												

<210> 94  
 <211> 743  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> HIV-1 gp120c trNef Tatm fusion

<400> 94

Met	Lys	Val	Lys	Glu	Thr	Arg	Lys	Asn	Tyr	Gln	His	Leu	Trp	Arg	Trp
1				5					10					15	
Gly	Thr	Met	Leu	Gly	Met	Leu	Met	Ile	Cys	Ser	Ala	Ala	Glu	Gln	
			20				25					30			
Leu	Trp	Val	Thr	Val	Tyr	Tyr	Gly	Val	Pro	Val	Trp	Lys	Glu	Ala	Thr
		35					40					45			
Thr	Thr	Leu	Phe	Cys	Ala	Ser	Asp	Ala	Lys	Ala	Tyr	Asp	Thr	Glu	Val
	50					55					60				
His	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr	Asp	Pro	Asn	Pro
65				70					75					80	
Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	Tyr	Phe	Asn	Met	Trp	Lys
				85					90					95	
Asn	Asn	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Leu	Trp	Asp
		100						105					110		
Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	Thr	Leu
		115					120					125			
Asp	Cys	Asp	Asp	Val	Asn	Thr	Thr	Asn	Ser	Thr	Thr	Thr	Thr	Ser	Asn
	130					135					140				
Gly	Trp	Thr	Gly	Glu	Ile	Arg	Lys	Gly	Glu	Ile	Lys	Asn	Cys	Ser	Phe
145					150					155					160
Asn	Ile	Thr	Thr	Ser	Ile	Arg	Asp	Lys	Val	Gln	Lys	Glu	Tyr	Ala	Leu
				165					170					175	
Phe	Tyr	Asn	Leu	Asp	Val	Val	Pro	Ile	Asp	Asp	Asp	Asn	Ala	Thr	Thr
		180						185					190		
Lys	Asn	Lys	Thr	Thr	Arg	Asn	Phe	Arg	Leu	Ile	His	Cys	Asn	Ser	Ser
		195					200					205			
Val	Met	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile
	210					215					220				
His	Tyr	Cys	Ala	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys
225					230					235					240
Thr	Phe	Asp	Gly	Lys	Gly	Leu	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys
				245					250					255	
Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly
			260					265					270		
Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp	Asn	Phe	Met	Asp
		275					280					285			
Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Ala	Ile	Asn
	290					295					300				
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile	His	Ile	Gly	Pro

## seqlist.txt

```

305      310      315      320
Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly Asp Ile Arg Gln
      325      330      335
Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn Thr Leu Lys Gln
      340      345      350
Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys Thr Ile Lys Phe
      355      360      365
Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg His Ser Phe Asn
      370      375      380
Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln Leu Phe Asn Ser
      385      390      395      400
Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly Asn Ser Thr Ile
      405      410      415
Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val
      420      425      430
Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln Ile Arg Cys Ser
      435      440      445
Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Thr Glu Gly
      450      455      460
Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp
      465      470      475      480
Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys
      485      490      495
Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Val Val
      500      505      510
Gln Arg Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro
      515      520      525
Met Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys
      530      535      540
Gly Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu
      545      550      555      560
Asp Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn
      565      570      575
Tyr Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys
      580      585      590
Tyr Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys
      595      600      605
Gly Glu Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp
      610      615      620
Asp Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala
      625      630      635      640
Phe His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys
      645      650      655
Thr Ser Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly
      660      665      670
Ser Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys
      675      680      685
Phe His Cys Gln Val Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr
      690      695      700
Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Gln Gly Ser Gln
      705      710      715      720
Thr His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly
      725      730      735
Glu Pro Thr Gly Pro Lys Glu
      740

```

&lt;210&gt; 95

&lt;211&gt; 1971

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; HIV-1 gp120c trNef fusion

&lt;400&gt; 95

```

atgaagggtca aggagaccag aaagaactac cagcatctgt ggcgctgggg caccatgctc 60
ctgggaatgc tgatgatctg ctccgccgcc gagcagctgt gggtcaccgt ctactacggc 120

```

seqlist.txt

```

gtgcctgtgt ggaaggaggc cacgaccacc ctcttctgcg cgagcgacgc caaggcctac 180
gacacggaag tgcataacgt gtgggcgacg catgcttgcg tgcctacgga ccccaacccc 240
caggaggtgg tgctgggaaa cgtgaccgag tacttcaaca tgtggaagaa taacatggtg 300
gatcagatgc acgaggacat catctctctg tgggaccagt cctgaagcc ctgctggaag 360
ctgacgcctc tctgctgac actggactgt gacgacgtca acaccaccaa cagcactacc 420
accaccagca acggctggac cggagagatt cgggaaggcg agatcaagaa ctgctccttc 480
aatatcacga cctcgatcag agacaagggt cagaaggaat acgcgctgtt ttataatctc 540
gatgtggtcc ccacgacga cgacaatgcc accaccaaga acaagacgac gcgtaatttc 600
agactcattc actgcaacag cagcgtcatg acgcaggcct gcccgaagggt gtccttcgaa 660
ccaatcccga tccattactg tgcccctgcc ggattcgcg taactcaagt taacaacaag 720
accttcgacg ggaagggcct gtgcaccaac gtcagcacgg tgcagtgcac ccattggcatc 780
cgccccgtcg tgagcaccca gctgctgctg aacgggtccc tggctgagga ggaggtggtg 840
atccggtcgg acaacttcat ggacaacacc aagacaatca tcgtccagct gaacgagtct 900
gtggcgatta actgtaccgg gcctaacaac aacaccgta agggcatcca catcgggcct 960
ggacgggcct tctatgccgc ccgcaagatc atcggcgaca tccggcaggc ccattgcaac 1020
ctctcccgcg cccagtggaa taacaccctg aagcagatcg tgatcaagct gagagagcac 1080
tttgaaaaca agaccatcaa gttcaatcag agttctggcg gagaccccga gatcgtgcgg 1140
cactccttca actgcggggg cgagttcttc tactgcgata cgacacagct cttcaactcc 1200
acctggaacg gcaccgaggg caacaacaca gagggaaact ccactatcac cctcccttgc 1260
cgcatcaagc agatcatcaa catgtggcag gaggtgggaa aggccatgta tgccccccc 1320
atcgggggccc agatccgctg ctctccaac atcaccggcc tgctgctcac cagagacggg 1380
ggcaccgagg gcaacggcac ggagaacgag acggagatct tcaggcccgg cggcggcgac 1440
atgagggata actggcggag cgagctgtac aagtacaagg tggggaagggt ggagccgctc 1500
ggcgtggccc ccaccggggc caagcgccgc gtcgtgcaga gaatggtggg tttccagtc 1560
acacctcagg tacctttaag accaatgact tacaaggcag ctgtagatct tagccacttt 1620
ttaaagaaa aggggggact ggaagggcta attcactccc aacgaagaca agatatactt 1680
gatctgtgga tctaccacac acaaggctac ttccctgatt ggcagaacta cacaccaggg 1740
ccaggggtca gatatccact gacctttgga tgggtctaca agctagtacc agttgagcca 1800
gataaggtag aagaggccaa taaaggagag aacaccagct tgttacaccc tgtgagcctg 1860
catggaatgg atgaccctga gagagaagtg ttagagtggg ggtttgacag ccgcctagca 1920
tttcatcacg tggcccgcga gctgcatccc gagtacttca agaactgcta a 1971

```

<210> 96

<211> 656

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 gp120c trNef fusion

<400> 96

```

Met Lys Val Lys Glu Thr Arg Lys Asn Tyr Gln His Leu Trp Arg Trp
 1          5          10          15
Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Ala Glu Gln
 20          25          30
Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
 35          40          45
Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val
 50          55          60
His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65          70          75          80
Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe Asn Met Trp Lys
 85          90          95
Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100          105          110
Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115          120          125
Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr Thr Ser Asn
130          135          140
Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe
145          150          155          160
Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu
165          170          175
Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp Asn Ala Thr Thr
180          185          190
Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His Cys Asn Ser Ser
195          200          205
Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile

```

## seqlist.txt

```

      210      215      220
His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys
225 230 235
Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser Thr Val Gln Cys
245 250 255
Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
260 265 270
Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp Asn Phe Met Asp
275 280 285
Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Ala Ile Asn
290 295 300
Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro
305 310 315
Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly Asp Ile Arg Gln
325 330 335
Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn Thr Leu Lys Gln
340 345 350
Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys Thr Ile Lys Phe
355 360 365
Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg His Ser Phe Asn
370 375 380
Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln Leu Phe Asn Ser
385 390 395
Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly Asn Ser Thr Ile
405 410 415
Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val
420 425 430
Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln Ile Arg Cys Ser
435 440 445
Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Thr Glu Gly
450 455 460
Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp
465 470 475
Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys
485 490 495
Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Val Val
500 505 510
Gln Arg Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro
515 520 525
Met Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys
530 535 540
Gly Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu
545 550 555
Asp Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn
565 570 575
Tyr Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys
580 585 590
Tyr Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys
595 600 605
Gly Glu Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp
610 615 620
Asp Pro Glu Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala
625 630 635
Phe His His Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys
645 650 655

```

```

<210> 97
<211> 3060
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> HIV-1 gp120c p17/24 trNef fusion

```

```

<400> 97
atgaagggtca aggagaccag aaagaactac cagcatctgt ggcgctgggg caccatgctc 60
ctgggaatgc tgatgatctg ctccgccgcc gagcagctgt gggtcaccgt ctactacggc 120
Page 72

```



seqlist.txt

```

gtgcctgtgt ggaaggaggc cacgaccacc ctcttctgcg cgagcgacgc caaggcctac 180
gacacggaag tgcataacgt gtgggcgacg catgcttgcg tgcctacgga ccccaacccc 240
caggaggtgg tgctgggaaa cgtgaccgag tacttcaaca tgtggaagaa taacatggtg 300
gatcagatgc acgaggacat catctctctg tgggaccagt cctgaagcc ctgctggaag 360
ctgacgcctc tctgctgac actggactgt gacgacgtca acaccaccaa cagcactacc 420
accaccagca acggctggac cggagagatt cggaaggcg agatcaagaa ctgctccttc 480
aatatcacga cctcgatcag agacaagggt cagaaggaat acgcgctgtt ttataatctc 540
gatgtggtcc ccacgcacga cgacaatgcc accaccaaga acaagacgac gcgtaatttc 600
agactcattc actgcaacag cagcgtcatg acgcaggcct gcccgaagg gtccttcgaa 660
ccaatcccgga tccattactg tgcccctgcc ggattcgcga tcctcaagt taacaacaag 720
accttcgacg ggaagggcct gtgcaccaac gtcagcacgg tgcagtgcac ccatggcatc 780
cgccccgtcg tgagcaccca gctgctgctg aacgggtccc tggctgagga ggaggtggtg 840
atccggtcgg acaacttcac ggacaacacc aagacaatca tcgtccagct gaacgagtct 900
gtggcgatta actgtaccgg gcctaacaac aacaccgta agggcatcca catcgggcct 960
ggacgggcct tctatgccgc ccgcaagatc atcggcgaca tccggcaggc ccattgcaac 1020
ctctcccgcg cccagtggaa taacaccctg aagcagatcg tgatcaagct gagagagcac 1080
tttggaaaca agaccatcaa gttcaatcac agttctggcg gagaccccga gatcgtgcgg 1140
cactccttca actgcggggg cgagttcttc tactgcgata cgacacagct cttcaactcc 1200
acctggaacg gcaccgaggg caacaacaca gagggaaact ccactatcac cctcccttgc 1260
cgcatcaagc agatcatcaa catgtggcag gaggtgggaa aggccatgta tgccccccc 1320
atcgggggccc agatccgctg ctctccaac atcaccggcc tgctgtcac cagagacggg 1380
ggcaccgagg gcaacggcac ggagaacgag acggagatct tcaggcccgg cggcggcgac 1440
atgagggata actggcgagg cgagctgtac aagtacaagg tggggaagg ggagccgctc 1500
ggcgtggccc ccaccgggc caagcgccgc gtcgtgcaga gaatgggtgc ccgagcttcg 1560
gtactgtctg gtggagagct ggacagatgg gagaaaatta ggctgcgccc gggaggcaaa 1620
aagaaatata agtcaagca tatcgtgtgg gcctcgaggg agcttgaacg gtttgccgtg 1680
aaccaggccc tgctggaaac atctgaggga tgtcgccaga tcctggggca attgcagcca 1740
tccctccaga ccgggagtga agagctgagg tccttgtata acacagtggc taccctctac 1800
tgcgtacacc agaggatcga gattaaggat accaaggagg ccttggaaca aattgaggag 1860
gagcaaaaca agagcaagaa gaagggcccag caggcagctg ctgacactgg gcatagcaac 1920
caggtatcac agaactatcc tattgtccaa aacattcagg gccagatggt tcatcaggcc 1980
atcaccccc ggacgctcaa tgcctgggtg aaggttgtcg aagagaaggc cttttctcct 2040
gaggttatcc ccatgttctc cgcttgagt gagggggcca ctctcagga cctcaataca 2100
atgcttaata ccgtgggccc ccatcaggcc gccatgcaaa tgttgaagga gactatcaac 2160
gaggaggcag ccgagtggga cagagtgcatt cccgtccacg ctggcccaat cgcgcccga 2220
cagatgcggg agcctcgcgg ctctgacatt gccggcacca cctctacact gcaagagcaa 2280
atcggatgga tgaccaacaa tcctcccac cagttggag aaatctataa acggtggatc 2340
attctcggtc tcaataaaat tgtagaatg tactctccga catccatcct tgacattaga 2400
cagggaccca aagagccttt tagggattac gtcgaccggt tttataagac cctgcgagca 2460
gagcaggcct ctcaggaggt caaaaactgg atgacggaga cactcctggt acagaacgct 2520
aaccgcgact gcaaaaacat ctgaaggcca ctaggcccgg ctgccaccct ggaagagatg 2580
atgaccgcct gtcagggagt aggcggaccc ggacacaaag ccagagtgtt gatggtgggt 2640
tttccagtca cacctcagg acctttaaga ccaatgactt acaaggcagc ttagatctt 2700
agccactttt taaaagaaaa ggggggactg gaagggctaa ttcactcca aagaagacaa 2760
gatattcctg atctgtggat ctaccacaca caaggctact tccctgattg gcagaactac 2820
acaccagggc caggggtcag atatccactg accttggat ggtgctacaa gctagtacca 2880
gttgagccag ataaggtaga agaggccaat aaaggagaga acaccagctt gttacaccct 2940
gtgagcctgc atgggatgga tgaccgggag agagaagtgt tagagtggag gtttgacagc 3000
cgcctagcat ttcatcacgt ggcccagag ctgcatccgg agtacttcaa gaactgctga 3060

```

<210> 98  
 <211> 1019  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> HIV-1 gp120c p17/24 trNef fusion

<400> 98  
 Met Lys Val Lys Glu Thr Arg Lys Asn Tyr Gln His Leu Trp Arg Trp  
 1 5 10 15  
 Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Ala Glu Gln  
 20 25 30  
 Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr  
 35 40 45  
 Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val  
 50 55 60

## seq1ist.txt

His 65	Asn	Val	Trp	Ala	Thr	His	Ala	Cys	Val	Pro	Thr	Asp	Pro	Asn	Pro
Gln	Glu	Val	Val	Leu	Gly	Asn	Val	Thr	Glu	Tyr	Phe	Asn	Met	Trp	Lys
Asn	Asn	Met	Val	Asp	Gln	Met	His	Glu	Asp	Ile	Ile	Ser	Leu	Trp	Asp
Gln	Ser	Leu	Lys	Pro	Cys	Val	Lys	Leu	Thr	Pro	Leu	Cys	Val	Thr	Leu
Asp	Cys	Asp	Asp	Val	Asn	Thr	Thr	Asn	Ser	Thr	Thr	Thr	Thr	Ser	Asn
Gly	Trp	Thr	Gly	Glu	Ile	Arg	Lys	Gly	Glu	Ile	Lys	Asn	Cys	Ser	Phe
Asn	Ile	Thr	Thr	Ser	Ile	Arg	Asp	Lys	Val	Gln	Lys	Glu	Tyr	Ala	Leu
Phe	Tyr	Asn	Leu	Asp	Val	Val	Pro	Ile	Asp	Asp	Asp	Asn	Ala	Thr	Thr
Lys	Asn	Lys	Thr	Thr	Arg	Asn	Phe	Arg	Leu	Ile	His	Cys	Asn	Ser	Ser
Val	Met	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile
His	Tyr	Cys	Ala	Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys
Thr	Phe	Asp	Gly	Lys	Gly	Leu	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys
Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly
Ser	Leu	Ala	Glu	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp	Asn	Phe	Met	Asp
Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Ala	Ile	Asn
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile	His	Ile	Gly	Pro
Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly	Asp	Ile	Arg	Gln
Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn	Thr	Leu	Lys	Gln
Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys	Thr	Ile	Lys	Phe
Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg	His	Ser	Phe	Asn
Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln	Leu	Phe	Asn	Ser
Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly	Asn	Ser	Thr	Ile
Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Asn	Met	Trp	Gln	Glu	Val	
Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln	Ile	Arg	Cys	Ser
Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Thr	Glu	Gly
Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro	Gly	Gly	Gly	Asp
Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys
Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys	Arg	Arg	Val	Val
Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly	Gly	Glu	Leu	Asp
Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Lys	Tyr	Lys
Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val
Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly
Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu
Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile

seqlist.txt

Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys
610						615					620				
Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn
625					630					635					640
Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met
				645					650					655	
Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val
			660					665					670		
Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala
		675					680					685			
Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr
	690					695					700				
Val	Gly	Gly	His	Gln	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	
705				710					715					720	
Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro
				725					730					735	
Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly
			740					745					750		
Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro
		755					760					765			
Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu
	770					775					780				
Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg
785					790					795					800
Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys
				805					810					815	
Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr
			820					825					830		
Glu	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu
		835					840					845			
Lys	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys
	850					855					860				
Gln	Gly	Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Met	Val	Gly
865					870					875					880
Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met	Thr	Tyr	Lys	Ala
				885					890					895	
Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly	Leu	Glu	Gly
			900					905					910		
Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp	Leu	Trp	Ile	Tyr
		915					920					925			
His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	Pro	Gly	Pro
	930					935					940				
Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys	Leu	Val	Pro
945					950					955					960
Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly	Glu	Asn	Thr	Ser
				965					970					975	
Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro	Glu	Arg	Glu
			980					985					990		
Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe	His	His	Val	Ala
		995					1000					1005			
Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys					
1010						1015									

<210> 99  
 <211> 3321  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 gp120c p17/24 trNef Tatm fusion

<400> 99  
 atgaaggtca aggagaccag aaagaactac cagcatctgt ggcgctgggg caccatgctc 60  
 ctgggaatgc tgatgatctg ctccgccgcc gagcagctgt gggtcaccgt ctactacggc 120  
 gtgccttgtt ggaaggaggc caccgaccacc ctcttctgcg cgagcgacgc caaggcctac 180  
 gacacggaag tgcataacgt gtgggagcag catgcttgcg tgcctacgga cccaacccc 240  
 caggaggtgg tgctgggaaa cgtgaccgag tacttcaaca tgtggaagaa taacatggtg 300

seqlist.txt

```

gatcagatgc acgaggacat catctctctg tgggaccagt ccctgaagcc ctgctgaag 360
ctgacgcctc tctgctgac actggactgt gacgacgtca acaccacca cagcactacc 420
accaccagca acggctggac cggagagatt cggagggcg agatcaagaa ctgctccttc 480
aatatcacga cctcgatcag agacaagggt cagaaggaa acgcgctgtt ttataatctc 540
gatgtggtcc ccacgcagca cgacaatgcc accaccaaga acaagacgac gcgtaatttc 600
agactcattc actgcaacag cagcgtcatg acgcaggcct gccccaaagt gtccttcgaa 660
ccaatcccga tccattactg tgcccctgcc ggattcgcga tcctcaagtg taacaacaag 720
accttcgacg ggaagggcct gtgcaccaac gtcagcacgg tgcagtgcac ccatggcatc 780
cgccccgtcg tgagacccca gctgctgctg aacgggtccc tggctgagga ggaggtggtg 840
atccggtcgg acaacttcat ggacaacacc aagacaatca tcgtccagct gaacgagtct 900
gtggcgatta actgtaccgc gcctaacaac aacaccgcgt agggcatcca catcgggcct 960
ggacgggcct tctatgccgc ccgcaagatc atcggcgaca tccggcaggc ccattgcaac 1020
ctctcccgcg cccagtggaa taacaccctg aagcagatcg tgatcaagct gagagagcac 1080
tttgaaaaca agaccatcaa gttcaatcag agttctggcg gagaccccga gatcgtgcgg 1140
cactccttca actgcggggg caacaacaca gagggaaact ccactatcac cctcccctgc 1260
acctggaacg gcaccgaggg catgtggcag gaggtgggaa aggccatgta tgccccccc 1320
cgcatcaagc agatccgctg ctctccaac acaccggcc tgcgtctcac cagagacggg 1380
atcggggggc agatccgctg ctctccaac acaccggcc tgcgtctcac cagagacggg 1440
ggcaccgagg gcaacggcac ggagaacgag acggagatct tcaggcccgg cggcggcgac 1500
atgagggata actggcggag cgagctgtac aagtacaagg tgggaagggt ggagccgctc 1560
ggcgtggccc ccacccgggc caagcggcg gtcgtgcaga gaatgggtgc ccgagcttcg 1620
gtactgtctg gtggagagtg ggacagatgg gagaaaatta ggctgcgccc gggaggcaaa 1680
aagaaataca agactaagca tatcgtgtgg gcctcgaggg agcttgaacg gtttgccgtg 1740
aaccaggccc tgctggaaac atctgagggg tgctgccaga tcctggggca attgcagcca 1800
tccctccaga ccgggagtg agagctgagg tccttgata acacagtggc taccctctac 1860
tgcgtacacc agaggatcga gattaaggat accaaggagg ccttgagcaa aattgaggag 1920
gagcaaaaca agagcaagaa gaaggcccg caggcagctg ctgacactgg gcatagcaac 1980
caggtatcac agaactatcc tattgtccaa aacattcagg gccagatggg tcatcaggcc 2040
atcagcccc ggacgtcaa tgccctgggtg aaggttgctg aagagaaggc cttttctcct 2100
gaggttatcc ccatgttctc cgctttagat gagggggcca ctctcagga cctcaataca 2160
atgcttaata ccgtggggcg ccatcaggcc gccatgcaaa tgttgaagga gactatcaac 2220
gaggagcgag ccgagtgagg cagagtgcac cccgtccacg ctggcccaat cgcgcccgga 2280
cagatcgagg agcctcgagg ctctgacatt gccggcacca cctctacact gcaagagcaa 2340
atcggatgga tgaccaacaa tcctcccatc ccagttggag aaatctataa acggtggatc 2400
attctcggtc tcaataaaa tgtagaatg tactctccga catccatcct tgacattaga 2460
cagggacca aagagccttt tagggattac gtcgaccggt tttataagac cctgcgagca 2520
gagcaggcct ctcaggaggt caaaaactgg atgacggaga cactcctggt acagaacgct 2580
aaccgcgact gcaaaacaat cttgaaggca ctaggcccgg ctgccaccct ggaagagatg 2640
atgaccgcct gtcaggaggt aggcggaccc ggacacaaag ccagagtgtt gatggtgggt 2700
tttccagtca cacctcaggt acctttaaga ccaatgactt acaaggcagc tgtagatctt 2760
agccactttt taaaagaaaa ggggggactg gaaggctaa ttcactccca acgaagacaa 2820
gatatacttg atctgtggat ctaccacaca caaggctact tccctgattg gcagaactac 2880
acaccagggc caggggtcag atatccactg accttggat ggtgctacaa gctagtacca 2940
gttgagccag ataaggtaga agaggccaat aaaggagaga acaccagctt gttacaccct 3000
gtgagcctgc attgaatgga tgaccctgag agagaagtgt tagagtggag gtttgacagc 3060
cgcctagcat ttcacacgt ggcccgagag ctgcattccg agtacttcaa gaactgcact 3120
agttagccag tagatcctag actagagccc tggaagcatc caggaagtca gcctaaaact 3180
gcttgtagca attgctattg taaaagtgt tgctttcatt gccagtttg tttcataaca 3240
gctgccttag gcatctccta tggcaggaag aagcggagac agcgacgaag acctcctcaa 3300
ggcagtcaga ctcatcaagt ttctctatca aagcaacca cctcccaatc caaaggggag 3321
ccgacaggcc cgaaggaata a

```

<210> 100

<211> 1106

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 gp120c p17/24 trNef Tatm fusion

<400> 100

```

Met Lys Val Lys Glu Thr Arg Lys Asn Tyr Gln His Leu Trp Arg Trp
1      5      10      15
Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Ala Glu Gln
20      25      30
Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
35      40      45
Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val

```

## seqlist.txt

50	His	Asn	Val	Trp	Ala	Thr	55	His	Ala	Cys	Val	60	Pro	Thr	Asp	Pro	Asn	Pro	
65	Gln	Glu	Val	Val	Leu	70	Gly	Asn	Val	Thr	Glu	75	Tyr	Phe	Asn	Met	Trp	80	Lys
					85		Gln	Met	His	Glu	Asp	90	Ile	Ile	Ser	Leu	95	Trp	Asp
	Asn	Asn	Met	Val	100	Asp	Pro	Cys	Val	Lys	105	Thr	Pro	Leu	Cys	110	Val	Thr	Leu
	Gln	Ser	Leu	Lys	115	Pro	Cys	Val	Lys	120	Thr	Asn	Ser	Thr	Thr	125	Thr	Ser	Asn
	Asp	Cys	Asp	Asp	Val	Asn	Thr	Thr	Thr	135	Thr	Asn	Ser	Thr	Thr	140	Thr	Ser	Asn
	Gly	Trp	Thr	Gly	Glu	Ile	150	Arg	Lys	Gly	Glu	Ile	155	Lys	Asn	Cys	Ser	Phe	160
145	Asn	Ile	Thr	Thr	Ser	165	Ile	Arg	Asp	Lys	Val	170	Gln	Lys	Glu	Tyr	Ala	Leu	175
	Phe	Tyr	Asn	Leu	180	Asp	Val	Val	Pro	Ile	Asp	185	Asp	Asp	Asp	Asn	Ala	Thr	Thr
	Lys	Asn	Lys	Thr	Thr	Arg	Asn	Phe	200	Arg	Leu	Ile	His	Cys	205	Asn	Ser	Ser	
	Val	Met	Thr	Gln	Ala	Cys	Pro	Lys	215	Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile		
	His	Tyr	Cys	Ala	Pro	Ala	230	Gly	Phe	Ala	Ile	Leu	235	Lys	Cys	Asn	Asn	Lys	240
225	Thr	Phe	Asp	Gly	Lys	245	Gly	Leu	Cys	Thr	Asn	Val	250	Ser	Thr	Val	Gln	Cys	255
	Thr	His	Gly	Ile	Arg	Pro	Val	Val	Ser	265	Thr	Gln	Leu	Leu	Leu	270	Asn	Gly	
	Ser	Leu	Ala	Glu	Glu	Val	Val	Ile	Arg	Ser	Asp	Asn	285	Phe	Met	Asp			
	Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser	300	Val	Ala	Ile	Asn		
	Cys	Thr	Arg	Pro	Asn	Asn	310	Asn	Thr	Arg	Lys	Gly	315	Ile	His	Ile	Gly	Pro	320
305	Gly	Arg	Ala	Phe	Tyr	Ala	325	Ala	Arg	Lys	Ile	Ile	330	Gly	Asp	Ile	Arg	Gln	335
	Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn	345	Thr	Leu	Lys	Gln		
	Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys	360	Thr	Ile	Lys	Phe		
	Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg	380	His	Ser	Phe	Asn		
	Cys	Gly	Gly	Glu	Phe	Phe	390	Tyr	Cys	Asp	Thr	Thr	395	Gln	Leu	Phe	Asn	Ser	400
385	Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly	410	Asn	Ser	Thr	Ile		
	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	425	Asn	Met	Trp	Gln	430	Glu	Val		
	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln	445	Ile	Arg	Cys	Ser		
	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	460	Gly	Thr	Glu	Gly		
	Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro	475	Gly	Gly	Gly	Asp		
465	Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	490	Lys	Val	Val	Lys		
	Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys	Arg	Arg	Val	Val			
	Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly	525	Gly	Glu	Leu	Asp		
	Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	540	Lys	Lys	Tyr	Lys		
	Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	555	Arg	Phe	Ala	Val		
545	Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	570	Gln	Ile	Leu	Gly		
	Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu			
	Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile			

## seqlist.txt

```

      595      600      605
Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys
610 615 620
Ser Lys Lys Lys Ala Gln Ala Ala Asp Thr Gly His Ser Asn
625 630 635 640
Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met
645 650 655
Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val
660 665 670
Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala
675 680 685
Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
690 695 700
Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn
705 710 715 720
Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro
725 730 735
Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly
740 745 750
Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro
755 760 765
Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu
770 775 780
Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg
785 790 795 800
Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys
805 810 815
Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr
820 825 830
Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu
835 840 845
Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys
850 855 860
Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Met Val Gly
865 870 875 880
Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala
885 890 895
Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly
900 905 910
Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr
915 920 925
His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro
930 935 940
Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro
945 950 955 960
Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser
965 970 975
Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu
980 985 990
Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His His Val Ala
995 1000 1005
Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser Glu Pro Val
1010 1015 1020
Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln Pro Lys Thr
1025 1030 1035 1040
Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His Cys Gln Val
1045 1050 1055
Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg
1060 1065 1070
Arg Gln Arg Arg Pro Pro Gln Gly Ser Gln Thr His Gln Val Ser
1075 1080 1085
Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro Thr Gly Pro
1090 1095 1100
Lys Glu
1105

```

## seqlist.txt

<211> 3513  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 gp120c p17/24 Nef Tatm fusion

<400> 101

atgaaggtca	aggagaccag	aaagaactac	cagcatctgt	ggcgctgggg	caccatgctc	60
ctgggaatgc	tgatgatctg	ctccgccgcc	gagcagctgt	gggtcacctg	ctactacggc	120
gtgccttgtg	ggaaggaggc	cacgaccacc	ctcttctgcg	cgagcgacgc	caaggcctac	180
gacacggaag	tgcataacgt	gtgggcgacg	catgcttgcg	tgcctacgga	ccccaacccc	240
caggaggtgg	tgtctggaaa	cgtgaccgag	tacttcaaca	tgtggaagaa	taacatggtg	300
gatcagatgc	acgaggacat	catctctctg	tgggaccagt	ccctgaagcc	ctgctggaag	360
ctgacgcctc	tctgctgac	actggactgt	gacgacgtca	acaccaccaa	cagcactacc	420
accaccagca	acggctggac	cggagagatt	cggaaagggcg	agatcaagaa	ctgctccttc	480
aatatcacga	cctcgatcag	agacaagggtg	cagaaggaat	acgcgctgtt	ttataatctc	540
gatgtggttc	ccatcgacga	cgacaatgcc	accaccaaga	acaagacgac	gcgtaatttc	600
agactcattc	actgcaacga	cagcgtcatg	accgaggcct	gccccaaagt	gtccttcgaa	660
ccaatcccga	tccattactg	tggccctgcc	ggattcgcga	tcctcaagtg	taacaacaag	720
accttcgacg	ggaagggcct	gtgcaccaac	gtcagcacgg	tgcagtgcac	ccatggcatc	780
cgccccgtcg	tgagcaccca	gctgctgctg	aacgggtccc	tggctgagga	ggaggtggtg	840
atccggtcgg	actgacattc	ggacaacacc	aagacaatca	tcgtccagct	gaacgagtct	900
gtggcgatta	actgtaccgg	gcctaacaac	aacaccgcta	agggcatcca	catcgggcct	960
ggacgggcct	tctatgccgc	ccgcaagatc	atcggcgaca	tccggcaggc	ccattgcaac	1020
ctctcccgcg	cccagtgga	taacaccctg	aagcagatcg	tgatcaagct	gagagagcac	1080
tttggaatac	agaccatcaa	gttcaatcag	agtcttggcg	gagaccccga	gatcgtgcgg	1140
cactccttca	actgcggggg	cgagtctctc	tactgcgata	cgacacagct	cttcaactcc	1200
acctggaacg	gcaccgaggg	caacaacaca	gagggaaact	ccactatcac	cctcccttgc	1260
cgcatcaagc	agatcatcaa	catgtggcag	gaggtgggaa	aggccatgta	tgcccccccc	1320
atcggggggc	agatccgctg	ctcctccaac	atcacgggcc	tgtgtgtcac	cagagacggg	1380
ggcaccgagg	gcaacggcac	ggagaacgag	acggagatct	tcaggcccgg	cggcggcgac	1440
atgagggata	actggcgag	cgagctgtac	aggtacaagg	tgggtgaagg	ggagccgctc	1500
ggcgtggccc	ccacccgggc	caagcgccgc	gtcgtgcaga	gaatgggtgc	ccgagcttcg	1560
gtactgtctg	gtggagagct	ggacagatgg	gagaaaatta	ggctgcgccc	gggaggcaaa	1620
aagaaatata	agctcaagca	tatcgtgtgg	gcctcgaggg	agcttgaacg	gtttgccgtg	1680
aacccaggcc	tgctggaaac	atctgagggg	tgctgccaga	tcctggggga	attgcagcca	1740
tccctccaga	ccgggagtga	agagctgagg	tccttgtata	acacagtggc	taccctctac	1800
tgcgtacacc	agaggatcga	gattaaggat	accaaggagg	ccttggaaca	aattgaggag	1860
gagcaaaaca	agagcaagaa	gaaggcccag	caggcagctg	ctgacactgg	gcatagcaac	1920
caggtatcac	agaactatcc	tattgtccaa	aacattcagg	gccagatggt	tcatacgacc	1980
atcacgcccc	ggacgctcaa	tgccctgggtg	aaggttgtcg	aagagaaggc	cttttctcct	2040
gaggttatcc	ccatgtttctc	cgctttgagt	gagggggcca	ctcctcagga	cctcaataca	2100
atgcttaata	ccgtgggcgg	ccatcaggcc	gccatgcaaa	tgttgaaagg	gactatcaac	2160
gaggaggcag	ccgagtggga	cagagtgcac	cccgtccacg	ctggcccaat	cgcgcccgga	2220
catagtgcgg	agcctcgcgg	ctctgacatt	cccggcacca	cctctacact	gcaagagcaa	2280
atcggatgga	tgaaccaaca	tcctcccac	ccagtggag	aaatctataa	acggtggatc	2340
attctcggtc	tcaataaaat	tgttagaatg	tactctccga	catccatcct	tgacattaga	2400
cagggaccca	aagagccttt	tagggattac	gtcgaccggt	tttataagac	cctgcgagca	2460
gagcaggcct	ctcaggaggt	caaaaactgg	atgacggaga	cactcctggt	acagaacgct	2520
aaccccagct	gcaaaacaat	cttgaaggca	ctaggcccgg	ctgccaccct	ggaagagatg	2580
atgaccgcct	gtcagggagt	aggcggaccc	ggacacaaag	ccagagtgtt	gatgggtggc	2640
aagtgggtcaa	aaagttagtgt	ggttggatgg	cctactgtaa	gggaaagaat	gagacgagct	2700
gagccagcag	cagatggggg	gggagcagca	tctcgagacc	tggaaaaaca	tggagcaatc	2760
acaagtagca	atacagcagc	taccaatgct	gcttgtgcct	ggctagaagc	acaagaggag	2820
gaggaggtgg	gttttccagt	cacacctcag	gtacccttaa	gaccaatgac	ttacaaggca	2880
gctgtagatc	ttagccactt	tttaaaagaa	aaggggggac	tggaaagggt	aattcactcc	2940
caacgaagac	aagatatcct	tgatctgtgg	atctaccaca	cacaaggcta	cttccctgat	3000
tggcagaact	acacaccagg	gccaggggtc	agatatccac	tgacctttgg	atggtgctac	3060
aagctagtac	cagttgagcc	agataaggta	gaagaggcca	ataaaggaga	gaacaccagc	3120
ttgttacacc	ctgtgagcct	gcattggaatg	gatgaccctg	agagagaagt	gttagagtgg	3180
aggtttgaca	gccgcctagc	atttcatcac	gtggcccagag	agctgcatcc	ggagtacttc	3240
aagaactgca	ctagttagcc	agtagatcct	agactagagc	cctggaagca	tccaggaagt	3300
cagcctaata	ctgcttgtac	caattgctat	tgtaaaaagt	gttgctttca	ttgccaagtt	3360
tgtttcataa	aggcatgcctt	tgatggcagg	tatggcagg	agaagcggag	acagcgacga	3420
agacctcctc	aaggcagtc	gactcatcaa	gtttctctat	caaagcaacc	cacctcccaa	3480
tccaaagggg	agccgacagg	cccgaaggaa	taa			3513

## seqlist.txt

<210> 102  
 <211> 1170  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> HIV-1 gp120c p17/24 Nef Tatm fusion

<400> 102  
 Met Lys Val Lys Glu Thr Arg Lys Asn Tyr Gln His Leu Trp Arg Trp  
 1 5 10 15  
 Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Ala Glu Gln  
 20 25 30  
 Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr  
 35 40 45  
 Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val  
 50 55 60  
 His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro  
 65 70 75 80  
 Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe Asn Met Trp Lys  
 85 90 95  
 Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp  
 100 105 110  
 Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu  
 115 120 125  
 Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr Thr Ser Asn  
 130 135 140  
 Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe  
 145 150 155 160  
 Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu  
 165 170 175  
 Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp Asn Ala Thr Thr  
 180 185 190  
 Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His Cys Asn Ser Ser  
 195 200 205  
 Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile  
 210 215 220  
 His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys  
 225 230 235 240  
 Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser Thr Val Gln Cys  
 245 250 255  
 Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly  
 260 265 270  
 Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp Asn Phe Met Asp  
 275 280 285  
 Asn Thr Lys Thr Ile Ile Val Gln Leu Asn Glu Ser Val Ala Ile Asn  
 290 295 300  
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Gly Ile His Ile Gly Pro  
 305 310 315 320  
 Gly Arg Ala Phe Tyr Ala Ala Arg Lys Ile Ile Gly Asp Ile Arg Gln  
 325 330 335  
 Ala His Cys Asn Leu Ser Arg Ala Gln Trp Asn Asn Thr Leu Lys Gln  
 340 345 350  
 Ile Val Ile Lys Leu Arg Glu His Phe Gly Asn Lys Thr Ile Lys Phe  
 355 360 365  
 Asn Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Arg His Ser Phe Asn  
 370 375 380  
 Cys Gly Gly Glu Phe Phe Tyr Cys Asp Thr Thr Gln Leu Phe Asn Ser  
 385 390 395 400  
 Thr Trp Asn Gly Thr Glu Gly Asn Asn Thr Glu Gly Asn Ser Thr Ile  
 405 410 415  
 Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln Glu Val  
 420 425 430  
 Gly Lys Ala Met Tyr Ala Pro Pro Ile Gly Gly Gln Ile Arg Cys Ser  
 435 440 445  
 Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Thr Glu Gly  
 450 455 460  
 Asn Gly Thr Glu Asn Glu Thr Glu Ile Phe Arg Pro Gly Gly Gly Asp



## seqlist.txt

```

465      470      475      480
Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys
485      490      495
Val Glu Pro Leu Gly Val Ala Pro Thr Arg Ala Lys Arg Arg Val Val
500      505      510
Gln Arg Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp
515      520      525
Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Tyr Lys
530      535      540
Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val
545      550      555      560
Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly
565      570      575
Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu
580      585      590
Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile
595      600      605
Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys
610      615      620
Ser Lys Lys Lys Ala Gln Gln Ala Ala Asp Thr Gly His Ser Asn
625      630      635      640
Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met
645      650      655
Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val
660      665      670
Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala
675      680      685
Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
690      695      700
Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn
705      710      715      720
Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro
725      730      735
Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly
740      745      750
Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro
755      760      765
Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu
770      775      780
Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg
785      790      795      800
Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys
805      810      815
Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr
820      825      830
Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu
835      840      845
Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys
850      855      860
Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Met Gly Gly
865      870      875      880
Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val Arg Glu Arg
885      890      895
Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala Ala Ser Arg
900      905      910
Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr Ala Ala Thr
915      920      925
Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu Glu Val Gly
930      935      940
Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala
945      950      955      960
Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly
965      970      975
Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr
980      985      990
His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro
995      1000      1005
Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro

```

seqlist.txt

```

1010      1015      1020
Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser
1025      1030      1035      1040
Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu
      1045      1050      1055
Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His His Val Ala
      1060      1065      1070
Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser Glu Pro Val
      1075      1080      1085
Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln Pro Lys Thr
      1090      1095      1100
Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His Cys Gln Val
1105      1110      1115      1120
Cys Phe Ile Thr Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg
      1125      1130      1135
Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His Gln Val Ser
      1140      1145      1150
Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro Thr Gly Pro
      1155      1160      1165
Lys Glu
1170

```

<210> 103  
 <211> 3513  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 gp120c p17/24 mL1-Nef Tatm fusion

```

<400> 103
atgaagggtca aggagaccag aaagaactac cagcatctgt ggcgctgggg caccatgctc 60
ctgggaatgc tgatgatctg ctccgccgcc gagcagctgt gggtcaccgt ctactacggc 120
gtgcctgtgt ggaaggaggc cacgaccacc ctcttctgcg cgagcgacgc caaggcctac 180
gacacggaag tgcataacgt gtgggcgacg catgcttgcg tgcctacgga cccaacccc 240
caggaggtgg tgctgggaaa cgtgaccgag tacttcaaca tgtggaagaa taacatgggtg 300
gatcagatgc acgaggacat catctctctg tgggaccagt ccctgaagcc ctgctgaag 360
ctgacgcctc tctgcgtgac actggactgt gacgacgtca acaccaccaa cagcactacc 420
accaccagca acggctggag cggagagatt cggaggggcg agatcaagaa ctgctccttc 480
aatatcacga cctcgcacag agacaagggt cagaaggaat acgcgctgtt ttataatctc 540
gatgtgtgtcc ccatcgacga cgacaatgcc accaccaaga acaagacgac gcgtaatttc 600
agactcattc actgcaacag cagcgtcatg acgcaggcct gccccaaagg gtctctcgaa 660
ccaattccga tccattactg tgcccctgcc ggattcgcga tcctcaagtg taacaacaag 720
accttcgacg ggaagggcct gtgcaccaac gtcagcacgg tgcagtgcac ccatggcatc 780
cgccccgtcg tgagcaccca gctgctgctg aacgggtccc tggctgagga ggaggtgggtg 840
atccggtcg acaacttcat ggacaacacc aagacaatca tcgtccagct gaacgagtct 900
gtggcgatta actgtaccgg gcctaacaac aacacccgta agggcatcca catcgggcct 960
ggacgggcct tctatgccgc ccgcaagatc atcggcgaca tccggcaggc ccattgcaac 1020
ctctcccgcg cccagtggaa taacaccctg aagcagatcg tgatcaagct gagagagcac 1080
tttgaaaaca agaccatcaa gttcaatcag agttctggcg gagaccccga gatcgtgcgg 1140
cactccttca actgcggggg cgagttcttc tactgcgata cgacacagct cttcaactcc 1200
acctggaacg gcaccgaggg caacaacaca gagggaaact ccactatcac cctcccttgc 1260
cgcatcaagc agatcatcaa catgtggcag gaggtgggaa aggccatgta tgcccccccc 1320
atcggggggc agatccgctg ctctccaac atcaccggcc tgctgctcac cagagacggg 1380
ggcaccgagg gcaacggcac ggagaacgag acggagatct tcaggcccgg cggcggcgac 1440
atgagggata actggcggag cgagctgtac aagtacaagg tgggtgaagg ggagccgctc 1500
ggcgtggccc ccaccggggc caagcgccgc gtcgtgcaga gaatgggtgc ccgagcttcg 1560
gtactgtctg gtggagagct ggacagatgg gagaaaatta ggctgcgccc gggaggcaaa 1620
aagaaataca agctcaagca tatcgtgtgg gctcggagg agcttgaacg gtttgccgtg 1680
aaccagggcc tgctggaaac atctgaggga tgtcgccaga tcctggggca attgcagcca 1740
tccctccaga ccgggagtga agagctgagg tccttgata acacagtggc taccctctac 1800
tgcgtaacac agaggatcga gattaaggat accaaggagg ccttggaaca aattgaggag 1860
gagcaaaaca gaagcaagaa gaaggccag caggcagctg ctgacactgg gcatagcaac 1920
caggatcac agaactatcc tattgtccaa aacattcagg gccagatggt tcatcagccc 1980
atcagcccc ggacgtcaa tgctgggtg aaggttgtcg aagagaaggc cttttctcct 2040
gaggttatcc ccattgtctc cgctttgagt gagggggcca ctctcagga cctcaatata 2100
atgcttaata ccgtgggcgg ccatcaggcc gccatgcaaa tgttgaagga gactatcaac 2160

```

seqlist.txt

```

gaggaggcag cccgagtggga cagagtgcac cccgtccacg ctggcccaat cgcgcccgga 2220
cagatgcggg agcctcgcgg ctctgacatt gccggcacca cctctacact gcaagagcaa 2280
atcggatgga tgaccaacaa tcctcccatc ccagttggag aaatctataa acggtggatc 2340
attctcggtc tcaataaaat tgtagaatg tactctccga catccatcct tgacattaga 2400
cagggaccca aagagccttt tagggattac gtcgaccggt ttataaagac cctgcgagca 2460
gagcaggcct ctcaggaggt caaaaactgg atgacggaga cactcctggt acagaacgct 2520
aaccgccgact gcaaaacaat cttgaaggca ctaggcccgg ctgccaccct ggaagagatg 2580
atgaccgcct gtcaggagggt aggcggaccc ggacacaaag ccagagtgtt gatgggtggc 2640
aagtgggtcaa aaagttagtgt ggttggtggt cctactgtaa gggaaagaat gagacgagct 2700
gagccagcag cagatgggggt gggagcagca tctcgagacc tggaaaaaca tggagcaatc 2760
acaagtagca atacagcagc taccaatgct gcttgtgcct ggctagaagc acaagaggag 2820
gaggaggtgg gttttccagt cacacctcag gtacctttta gaccaatgac ttacaaggca 2880
gctgtagatc ttagccactt tttaaaagaa aaggggggac tggaagggct aattcactcc 2940
caacgaagac aagatatcct tgatctgtgg atctaccaca cacaaggcta cttccctgat 3000
tggcagaact acacaccagg gccaggggtc agatatccac tgacctttgg atggtgctac 3060
aagctagtac cagttgagcc agataaggta gaagaggcca ataaaggaga gaacaccagc 3120
gccttacacc ctgtgagcct gcatggaatg gatgaccctg agagagaagt gttagagtgg 3180
aggtttgaca gccgcctagc atttcacac agtggccgag agctgcatcc ggagtacttc 3240
aagaactgca ctagtgagcc agtagatcct agactagagc cctggaagca tccaggaagt 3300
cagcctaaaa ctgcttgtag caattgctat tgtaaaaagt gttgctttca ttgccaagtt 3360
tgtttcataa cagctgcctt aggcattctc tatggcagga agaagcggag acagcgacga 3420
agacctcttc aaggcagtca gactcatcaa gtttctctat caaagcaacc cacctcccaa 3480
tccaaagggg agccgacagg cccgaaggaa taa 3513

```

<210> 104

<211> 1170

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 gp120c p17/24 mL1-Nef Tatm fusion

<400> 104

```

Met Lys Val Lys Glu Thr Arg Lys Asn Tyr Gln His Leu Trp Arg Trp
 1      5      10      15
Gly Thr Met Leu Leu Gly Met Leu Met Ile Cys Ser Ala Ala Glu Gln
 20      25      30
Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
 35      40      45
Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu Val
 50      55      60
His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65      70      75      80
Gln Glu Val Val Leu Gly Asn Val Thr Glu Tyr Phe Asn Met Trp Lys
 85      90      95
Asn Asn Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100      105      110
Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115      120      125
Asp Cys Asp Asp Val Asn Thr Thr Asn Ser Thr Thr Thr Ser Asn
130      135      140
Gly Trp Thr Gly Glu Ile Arg Lys Gly Glu Ile Lys Asn Cys Ser Phe
145      150      155      160
Asn Ile Thr Thr Ser Ile Arg Asp Lys Val Gln Lys Glu Tyr Ala Leu
165      170      175
Phe Tyr Asn Leu Asp Val Val Pro Ile Asp Asp Asp Asn Ala Thr Thr
180      185      190
Lys Asn Lys Thr Thr Arg Asn Phe Arg Leu Ile His Cys Asn Ser Ser
195      200      205
Val Met Thr Gln Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile
210      215      220
His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys
225      230      235      240
Thr Phe Asp Gly Lys Gly Leu Cys Thr Asn Val Ser Thr Val Gln Cys
245      250      255
Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly
260      265      270
Ser Leu Ala Glu Glu Glu Val Val Ile Arg Ser Asp Asn Phe Met Asp

```

## seqlist.txt

Asn	Thr	Lys	Thr	Ile	Ile	Val	Gln	Leu	Asn	Glu	Ser	Val	Ala	Ile	Asn
	290					295					300				
Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly	Ile	His	Ile	Gly	Pro
305					310					315					320
Gly	Arg	Ala	Phe	Tyr	Ala	Ala	Arg	Lys	Ile	Ile	Gly	Asp	Ile	Arg	Gln
				325					330					335	
Ala	His	Cys	Asn	Leu	Ser	Arg	Ala	Gln	Trp	Asn	Asn	Thr	Leu	Lys	Gln
			340					345					350		
Ile	Val	Ile	Lys	Leu	Arg	Glu	His	Phe	Gly	Asn	Lys	Thr	Ile	Lys	Phe
		355					360					365			
Asn	Gln	Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Arg	His	Ser	Phe	Asn
	370					375					380				
Cys	Gly	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Thr	Gln	Leu	Phe	Asn	Ser
385					390					395					400
Thr	Trp	Asn	Gly	Thr	Glu	Gly	Asn	Asn	Thr	Glu	Gly	Asn	Ser	Thr	Ile
				405					410					415	
Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Asn	Met	Trp	Gln	Glu	Val	
			420					425				430			
Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Gly	Gly	Gln	Ile	Arg	Cys	Ser
		435					440					445			
Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	Thr	Glu	Gly
	450					455					460				
Asn	Gly	Thr	Glu	Asn	Glu	Thr	Glu	Ile	Phe	Arg	Pro	Gly	Gly	Gly	Asp
465					470				475						480
Met	Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys
				485					490					495	
Val	Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Arg	Ala	Lys	Arg	Arg	Val	Val
			500					505					510		
Gln	Arg	Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly	Gly	Glu	Leu	Asp
		515					520					525			
Arg	Trp	Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Lys	Tyr	Lys
	530					535					540				
Leu	Lys	His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val
545					550					555					560
Asn	Pro	Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly
				565					570					575	
Gln	Leu	Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu
			580					585					590		
Tyr	Asn	Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile
		595					600					605			
Lys	Asp	Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys
	610					615					620				
Ser	Lys	Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn
625					630					635					640
Gln	Val	Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met
				645					650					655	
Val	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val
			660					665					670		
Val	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala
		675					680					685			
Leu	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr
	690					695					700				
Val	Gly	Gly	His	Gln	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	
705					710					715					720
Glu	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro
				725					730					735	
Ile	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly
			740					745					750		
Thr	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro
		755					760					765			
Pro	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu
	770					775					780				
Asn	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg
785					790					795					800
Gln	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys
				805					810					815	
Thr	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr

## seqlist.txt

820 825 830  
 Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu  
 835 840 845  
 Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys  
 850 855 860  
 Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Met Gly Gly  
 865 870 875  
 Lys Trp Ser Lys Ser Val Val Gly Trp Pro Thr Val Arg Glu Arg  
 885 890 895  
 Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala Ala Ser Arg  
 900 905 910  
 Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr Ala Ala Thr  
 915 920 925  
 Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu Glu Val Gly  
 930 935 940  
 Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala  
 945 950 955  
 Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly  
 965 970 975  
 Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr  
 980 985 990  
 His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro  
 995 1000 1005  
 Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro  
 1010 1015 1020  
 Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser  
 1025 1030 1035  
 Ala Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu  
 1045 1050 1055  
 Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His His Val Ala  
 1060 1065 1070  
 Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser Glu Pro Val  
 1075 1080 1085  
 Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln Pro Lys Thr  
 1090 1095 1100  
 Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His Cys Gln Val  
 1105 1110 1115  
 Cys Phe Ile Thr Ala Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg  
 1125 1130 1135  
 Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His Gln Val Ser  
 1140 1145 1150  
 Leu Ser Lys Gln Pro Thr Ser Gln Ser Lys Gly Glu Pro Thr Gly Pro  
 1155 1160 1165  
 Lys Glu  
 1170

<210> 105  
 <211> 3204  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> HIV-1 RT Nef p17/24 fusion

<400> 105  
 atgggccccca tcagtcccat cgagaccgtg ccggtgaagc tgaaacccgg gatggacggc 60  
 cccaaggtca agcagtggcc actcaccgag gagaagatca aggccctggt ggagatctgc 120  
 accgagatgg agaaagaggg caagatcagc aagatcgggc ctgagaaccc atacaacacc 180  
 cccgtgtttg ccatcaagaa gaaggacagc accaagtggc gcaagctggt ggatttccgg 240  
 gagctgaata agcggaccca ggatttctgg gaggtccagc tgggcatccc ccatccggcc 300  
 ggcctgaaga agaagaagag cgtgaccgtg ctggacgtgg gcgacgctta cttcagcgtc 360  
 cctctggacg aggacttttag aaagtacacc gcctttacca tcccatctat caacaacgag 420  
 acccctggca tcagatatca gtacaacgtc ctccccagg gctggaaggg ctctcccgcc 480  
 attttccaga gctccatgac caagatcctg gagccgtttc ggaagcagaa ccccgatatc 540  
 gtcattctacc agtacatgga cgacctgtac gtgggctctg acctggaat cgggcagcat 600  
 cgcacgaaga ttgaggagct gaggcagcat ctgctgagat ggggcctgac cactccggac 660  
 aagaagcatc agaaggagcc gccattcctg aagatgggct acgagctcca tcccagacaag 720

# seqlist.txt

```

tggaccgtgc agcctatcgt cctccccgag aaggacagct ggaccgtgaa cgacatccag 780
aagctggtgg gcaagctcaa ctgggctagc cagatctatc ccgggatcaa ggtgcccag 840
ctctgcaagc tgctgcgcgg caccaaggcc ctgaccgagg tgattcccct cacggaggaa 900
gccgagctcg agctggctga gaaccgggag atcctgaagg agcccgtgca cggcgtgtac 960
tatgacctct ccaaggacct gatcgccgaa atccagaagc agggccaggg gcagtggaca 1020
taccagattt accaggagcc tttcaagaac ctcaagaccg gcaagtacgc ccgcatgagg 1080
ggcgcccaca ccaacgatgt caagcagctg accgaggccg tccagaagat cacgaccgag 1140
tccatcgtga tctgggggaa gacacccaag ttcaagctgc ctatccagaa ggagacctgg 1200
gagacgtggt ggaccgaata ttggcaggcc acctggattc ccgagtggga gttcgtgaat 1260
acacctcttc tgggtgaagct gtggtaccag ctcgagaagg agcccatcgt gggcgcggag 1320
acattctacg tggacggcgc ggccaaccgc gaaacaaagc tcgggaaggc cgggtacgtc 1380
accaaccggg gccgcccagaa ggtcgtcacc ctgaccgaca ccaccaacca gaagacggag 1440
ctgcaggcca tctatctcgc tctccaggac tccggcctgg aggtgaacat cgtgacggac 1500
agccagtacg cgctgggcat tattcaggcc cagccggacc agtccgagag cgaactggtg 1560
aaccagatta tcgagcagct gatcaagaaa gagaaggctt acctcgcttg ggtcccggcc 1620
cataagggca ttggcggaat cgagcaggtc gacaagctgg tgagtgcggg gattagaaag 1680
gtgctgatgg tgggttttcc agtcacacct cagggtacct taagaccaat gacttacaag 1740
gcagctgtag atttttaaaa gaaaaggggg gactggaagg gctaattcac 1800
tcccaaagaa gacaagatat ccttgatctg tggatctacc acacacaagg ctacttcctt 1860
gattggcaga actacacacc agggccaggg gtcagatatc cactgacctt tggatggtgc 1920
tacaagctag taccagttga gccagataag gtagaagagg ccaataaagg agagaacacc 1980
agcttggtac accctgtgag cctgcattgg atggatgacc cggagagaga agtggttagag 2040
tggagtttgg acagccgctt agcatttcct cacgtggccc gagagctgca tccggagtag 2100
ttcaagaact gcatgggtgc ccgagcttcg gtactgtctg gtggagagct ggacagatgg 2160
gagaaaatta ggctgcgccc gggaggcaaa aagaaatata agctcaagca tatcgtgtgg 2220
gcctcgaggg agcttgaacg gtttgccgtg aaccaggccc tgctggaaac atctgaggga 2280
tgctgccaga tcctggggca attgcagcca tccctccaga ccgggagtga agagctgagg 2340
tccttgata acacagtggc tacctcttac tgcgtacacc agaggatcga gattaaggat 2400
accaaggagg ccttgacaaa aattgaggag gagcaaaaca agagcaagaa gaaggcccag 2460
caggcagctg ctgacactgg gcatagcaac caggtatcac agaactatcc tattgtccaa 2520
aacattcagg gccagatggt tcatcaggcc atcagcccc ggacgctcaa tgcctgggtg 2580
aagggtgtcg aagagaaggc cttttctcct gaggttatcc ccatgttctc cgctttgagt 2640
gagggggcca ctctcagga cctcaatata atgtttaata ccgtgggcgg ccacaggcc 2700
gccatgcaaa tgttgaaagg gactatcaac gaggaggcag ccgagtggga cagagtgcatt 2760
cccgtccacg ctggcccaat cgcgcccga cagatgcggg agcctcgcg ctctgacatt 2820
gccggcacca cctctacact gcaagagcaa atcggatgga tgaccaacaa tcctcccatc 2880
ccagttggag aaatctataa acggtggatc atcgtgggcc tgaacaagat cgtgcgcatt 2940
tactctccga catccatcct tgacattaga cagggaccca aagagccttt tagggattac 3000
gtcgaccggt tttataagac cctgcgagca gagcaggcct ctgaggagg caaaaactgg 3060
atgacggaga cactcctggt acagaacgct aaccccgact gcaaaacaat cttgaaggca 3120
ctaggcccgg ctgccaccct ggaagagatg atgaccgcct gtcagggagt aggcggacc 3180
ggacacaag ccagagtgtt gtaa

```

<210> 106

<211> 1067

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV-1 RT Nef p17/24 fusion

<400> 106

```

Met Gly Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro
1      5      10      15
Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Lys
20     25     30
Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys
35     40     45
Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala
50     55     60
Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg
65     70     75     80
Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
85     90     95
Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp
100    105    110
Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys
115    120    125

```

## seqlist.txt

```

Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile
130 135
Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala
145 150
Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln
165 170
Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly
180 185
Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg
195 200
Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln
210 215
Lys Glu Pro Pro Phe Leu Lys Met Gly Tyr Glu Leu His Pro Asp Lys
225 230
Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val
245 250
Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
260 265
Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr
275 280
Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu
290 295
Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
305 310
Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
325 330
Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
340 345
Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
355 360
Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile
370 375
Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp
385 390
Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp
405 410
Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu
420 425
Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala
435 440
Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly
450 455
Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu
465 470
Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn
485 490
Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro
500 505
Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile
515 520
Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile
530 535
Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys
545 550
Val Leu Met Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro
565 570
Met Thr Tyr Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys
580 585
Gly Gly Leu Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu
595 600
Asp Leu Trp Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn
610 615
Tyr Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys
625 630
Tyr Lys Leu Val Pro Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys
645 650
Gly Glu Asn Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp
660 665 670

```

seqlist.txt

Asp	Pro	Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala
		675					680					685			
Phe	His	His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys
		690				695					700				
Met	Gly	Ala	Arg	Ala	Ser	Val	Leu	Ser	Gly	Gly	Glu	Leu	Asp	Arg	Trp
705					710					715					720
Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Lys	Tyr	Lys	Leu	Lys
				725					730					735	
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro
			740					745					750		
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu
		755					760					765			
Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn
		770				775					780				
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile	Lys	Asp
785					790					795					800
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Gln	Asn	Lys	Ser	Lys	
				805					810					815	
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Asn	Gln	Val
			820					825					830		
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His
		835					840					845			
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
		850				855					860				
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser
865					870					875					880
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly
				885					890					895	
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu
			900					905					910		
Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala
		915					920					925			
Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr
		930				935					940				
Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	Ile
945					950					955					960
Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys
				965					970					975	
Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly
			980					985					990		
Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu
		995					1000					1005			
Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr
						1015					1020				
Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala
1025					1030					1035					1040
Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly
				1045					1050					1055	
Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu					
			1060					1065							